

83215 seq

85121 Text

Access DB# \_\_\_\_\_

**SEARCH REQUEST FORM**

Scientific and Technical Information Center

Requester's Full Name: SHANNON TERRY Examiner #: 77531 Date: 1/21/03  
 Art Unit: 1608 Phone Number 30 8 3053 Serial Number: 17000007  
 Mail Box and Bldg/Room Location: 8112/2009 Results Format Preferred (circle): PAPER DISK E-MAIL

**If more than one search is submitted, please prioritize searches in order of need.**

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Method of measuringInventors (please provide full names): Shannon TerryEarliest Priority Filing Date: 12/11/02

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

51d 50 515 50 515 515  
 Please search 511 104 42 (same as 511 379)  
 and any out body that leads to any patent at 511 104 42

111 111

10 10 mo. c  
STN

111

Please also include an interference search.

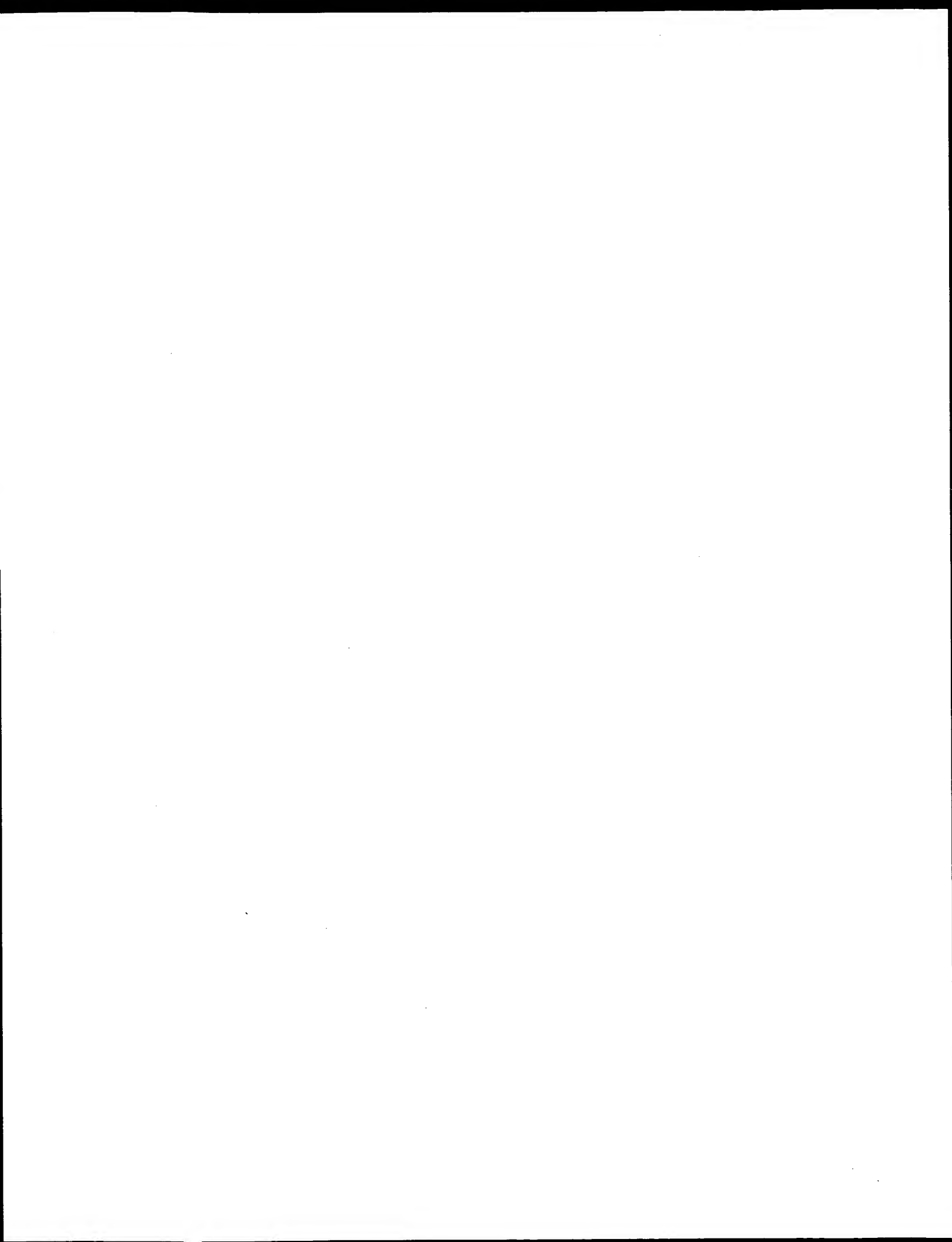
Please search for serial 511 104 42.

AK 2-379

BEST AVAILABLE COPY

\*\*\*\*\*  
**STAFF USE ONLY****Type of Search****Vendors and cost where applicable**

Searcher: D. S. L. E. D. W. NA Sequence (#) \_\_\_\_\_ STN 129, 89  
 Searcher Phone #: 308-4200 AA Sequence (#) 14 Dialog \_\_\_\_\_  
 Searcher Location: CM 6A03 Structure (#) \_\_\_\_\_ Questel/Orbit \_\_\_\_\_  
 Date Searcher Picked Up: \_\_\_\_\_ Bibliographic \_\_\_\_\_ Dr. Link \_\_\_\_\_  
 Date Completed: 1/24/03 Litigation \_\_\_\_\_ Lexis/Nexis \_\_\_\_\_  
 Searcher Prep & Review Time: 10/30 Fulltext \_\_\_\_\_ Sequence Systems Comp  
 Clerical Prep Time: \_\_\_\_\_ Patent Family \_\_\_\_\_ WWW/Internet \_\_\_\_\_  
 Online Time: 10/30 Other \_\_\_\_\_ Other (specify) \_\_\_\_\_



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run On: January 24, 2003, 12:21:10 ; Search time 37 Seconds  
(without alignments)  
1364.919 Million cell updates/sec

Title: US-09-944-457-2  
Perfect score: 1992  
Sequence: 1 MKEVLLLLFALCSAKPFFS.....PATFRCVLSRMSVQLGNFGM 379

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : A\_Geneseq\_101002.\*  
1: /SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
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22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1992	100.0	379	21	Human PRO241 polyp
2	1992	100.0	379	22	Human PRO241 polyp
3	1992	100.0	379	23	Human angiogenesis
4	1992	100.0	379	23	Human PRO241 prote
5	1990	99.9	379	20	Human PRO241 prote
6	1799	90.3	373	22	Mouse bone/cartila
7	1799	90.3	373	23	Murine protein iso
8	1649	82.8	344	22	Human polypeptide
9	1558	78.2	352	22	Novel human diagno
10	1237	62.1	245	22	Human protein sequ

11	1040.5	52.2	369	16	AAB87951	Rat neurotrophic b
12	1034	51.9	368	22	AAB85043	Human biglycan pro
13	1031.5	51.8	369	16	AAB87952	Human neurotrophic
14	1021	51.3	368	22	AAG78510	Human biglycan ami
15	1020	51.2	368	11	AAR05159	Sequence of human
16	1015	51.0	332	16	AAR87953	Bovine neurotroph
17	1007	50.6	197	22	AA42137	Human polypeptide
18	963.5	48.4	359	21	AA57079	Human decorin amin
19	963.5	48.4	359	22	AA78511	Human decorin amin
20	963.5	48.4	360	22	AA087286	Novel central nerv
21	949	47.6	342	17	AAR89439	Human recombinant
22	947	47.5	331	14	AA42260	Mature decorin PT-
23	947	47.5	1388	17	AAR89471	Collagen/decorin f
24	947	47.5	1388	21	AA784539	Amino acid sequenc
25	907	45.5	353	11	AAR05160	Sequence of human
26	847	42.5	305	14	AA42267	Decorin sequence p
27	793.5	39.8	423	22	AAU30348	Novel human secret
28	776	39.0	280	14	AA42266	Decorin sequence p
29	643	32.3	128	22	AAU20404	Human secreted pro
30	616	30.9	234	14	AA42265	Decorin sequence p
31	493	24.7	88	21	AA00241	Human secreted pro
32	493	24.7	88	21	AA564720	Human 5' EST relat
33	493	24.7	186	14	AA42264	Decorin sequence p
34	433	21.7	146	20	AA59749	Human normal ovari
35	406.5	20.4	155	21	AA44116	Human cancer assoc
36	397.5	20.0	699	21	AA57598	Human adipose tiss
37	393	19.7	353	21	AA43535	Human cancer assoc
38	390	19.6	338	23	ABB90763	Human Tumour Endot
39	390	19.6	353	22	AA73881	Human colon cancer
40	384.5	19.3	139	14	AA42263	Decorin sequence p
41	366	18.4	421	20	AA05767	Human osteomodulin
42	366	18.4	421	21	AA33417	Human PRO216 prote
43	366	18.4	421	21	AA24435	Human PRO216 prote
44	366	18.4	421	21	AA58377	PRO216 (osteomodul
45	366	18.4	421	22	AAU12322	Human PRO216 polyp
46	366	18.4	421	22	AA20340	Human PRO216. Hom
47	366	18.4	421	23	AAU81955	Human PRO216. Hom
48	366	18.4	772	22	AB812438	Human bone marrow
49	363.5	18.2	674	22	AA40226	Human polypeptide
50	363.5	18.2	674	22	AAU12189	Human PRO1483 poly

#### ALIGNMENTS

RESULT 1  
AAB01311  
ID AAB01311 standard; Protein; 379 AA.  
XX  
AC AAB01311;  
XX  
DT 25-SEP-2000 (first entry)  
XX  
DE Human PRO241 polypeptide.  
XX  
KW PRO; membrane bound protein; secreted protein; PRO357; PRO327;  
PRO243; PRO715; PRO243; PRO323; PRO299; PRO344; PRO347;  
PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide;  
antibody; screening; detection; inhibition; primer; human.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..15 /label= Signal peptide  
FT Modified-site 129..135 /note= "N-myristoylation site"  
FT Domain 134..176 /label= Leucine zipper pattern  
FT Modified-site 210..216 /note= "N-myristoylation site"  
FT Modified-site 214..220 /note= "N-myristoylation site"

FT Modified-site 214..220 /note= "N-myristoylation site"  
 FT Modified-site 237..243 /note= "N-myristoylation site"  
 FT Modified-site 270..276 /note= "N-myristoylation site"  
 FT Modified-site 281..285 /note= "N-myristoylation site"  
 FT Modified-site 282..288 /note= "N-glycosylation site"  
 FT Modified-site /note= "N-myristoylation site"  
 XX WO200032776-A2.  
 PN 08-JUN-2000.  
 XX 01-DEC-1999; 99WO-US28301.  
 XX 01-DEC-1998; 98WO-US25108.  
 PR 16-DEC-1998; 98US-0112850.  
 PR 22-DEC-1998; 98US-0113296.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;  
 PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;  
 PI Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;  
 XX  
 DR WPI: 2000-412324/35.  
 DR N-PSDB: AAA49551.  
 XX  
 PT New human nucleic acids encoding secreted and transmembrane  
 PT polypeptides, designated as PRO polypeptides, useful as pharmaceutical  
 PT and diagnostic agents  
 XX  
 PS Claim 12; Fig 2; 187pp; English.  
 XX  
 CC New human nucleic acids encoding secreted and transmembrane  
 CC polypeptides which are designated as PRO polypeptides are described  
 CC The membrane-bound proteins have various industrial applications,  
 CC including as pharmaceutical and diagnostic agents. The membrane-bound  
 CC proteins can also be employed for screening of potential peptide or  
 CC small molecule inhibitors of the relevant receptor/ligand interaction.  
 CC Anti-PRO antibodies are useful for the affinity purification of PRO  
 CC from recombinant cell culture or natural sources.  
 XX  
 SQ Sequence 379 AA;  
 Query Match 100.0%; Score 1992; DB 21; Length 379;  
 Best Local Similarity 100.0%; Pred. No. 4e-177;  
 Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKEYVLLFLALCSAKFPFSPSHALKNMMLKDMEDTDDDDDDDDDDNSLFPPTRE 60  
 DB 1 MKEYVLLFLALCSAKFPFSPSHALKNMMLKDMEDTDDDDDDDDDDNSLFPPTRE 60  
 QY 61 PRSHFFPDLFPMCPFGCQYSRVHCSDLGLTSVPTNIPDTRMLDLQNNKIKEIKEND 120  
 DB 61 PRSHFFPDLFPMCPFGCQYSRVHCSDLGLTSVPTNIPDTRMLDLQNNKIKEIKEND 120  
 QY 121 PKGLTSLGLIINNNKLTIKHPKAFLTTKLRLRLYLSHNSQLSEIPLNPKSLAEIRIHEN 180  
 DB 121 PKGLTSLGLIINNNKLTIKHPKAFLTTKLRLRLYLSHNSQLSEIPLNPKSLAEIRIHEN 180  
 QY 181 KYVKTQKDTFGMNAHVLENSANPLDNNNGIEPGAFEGVTVFHRIAEAKLTSPKGLIPP 240  
 DB 181 KYVKTQKDTFGMNAHVLENSANPLDNNNGIEPGAFEGVTVFHRIAEAKLTSPKGLIPP 240  
 QY 241 TLELHLDYNNKISTVELEDFRYKELQRLGLGNKNTDIENGSLANIPRVREIHLNNKL 300  
 DB 241 TLELHLDYNNKISTVELEDFRYKELQRLGLGNKNTDIENGSLANIPRVREIHLNNKL 300  
 QY 301 KKIPSGLPKLYLOTIFUHSNRIARVGVNDFCPTVPKMKKSLYSALSIFNNPVKYWEMOP 360  
 DB 301 KKIPSGLPKLYLOTIFUHSNRIARVGVNDFCPTVPKMKKSLYSALSIFNNPVKYWEMOP 360  
 Db 301 KKIPSGLPKLYLOTIFUHSNRIARVGVNDFCPTVPKMKKSLYSALSIFNNPVKYWEMOP 360  
 QY 361 ATRFCVLSRMSVOLGNFGM 379  
 Db 361 ATRFCVLSRMSVOLGNFGM 379  
 RESULT 2  
 AAU12335  
 ID AAU12335 standard; Protein; 379 AA.  
 XX  
 AC AAU12335;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Human PRO241 polypeptide sequence.  
 XX  
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;  
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;  
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;  
 KW adipocyte; A-peptide; factor VIIA; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200140466-A2.  
 XX  
 PD 07-JUN-2001.  
 XX  
 PF 01-DEC-2000; 2000WO-US32678.  
 XX  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 09-DEC-1999; 99US-0170262.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 16-DEC-1999; 99WO-US30911.  
 PR 20-DEC-1999; 99WO-US30999.  
 PR 30-DEC-1999; 99WO-US31243.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 01-MAR-2000; 2000WO-US05601.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 10-NOV-2000; 2000WO-US30873.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI: 2001-408281/43.  
 DR N-PSDB: AAS21407.  
 XX  
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect  
 PT other PRO polypeptides, link bioactive molecules to cells expressing  
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.  
 PT lung, breast, prostate, cervical  
 XX  
 PS Claim 12; Fig 328; 813pp; English.



XX AAU12172-AAU12446 represent novel human secretory and transmembrane  
 CC PRO polypeptides. The PRO polypeptides are useful to detect other  
 CC PRO polypeptides, to link bioactive molecules to cells expressing  
 CC PRO polypeptides, to modulate biological activities of cells expressing  
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,  
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
 CC polypeptide expression in a cell sample to that in a control sample.  
 CC Some of the 275 sequences are also useful to stimulate the release of  
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the  
 CC proliferation or differentiation of chondrocytes, the proliferation or  
 CC gene expression in pericyte cells, the release of proteoglycans from  
 CC cartilage, the proliferation of inner ear utricular supporting cells or  
 CC of T-lymphocytes, the release of a cytokine from peripheral blood  
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of  
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by  
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide  
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify  
 CC molecules involved in binding interactions. The polynucleotides encoding  
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,  
 CC transgenic or knock out animals and can be used in gene therapy.  
 XX

Sequence 379 AA;  
 Query Match 100.0%; Score 1992; DB 22; Length 379;  
 Best Local Similarity 100.0%; Pred. No. 4e-177;  
 Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 MKEYVLLFLALCSAKPFPSHIALKNMMLKDMEDTDDDDDDDDDDDDSLFPFRE 60

QY 61 PRSHFFPDLPMCPFGQCYSRVVHCSDLGLTSVPTNIPDTRMLDLQNNKIKEIKEND 120  
 Db 61 PRSHFFPDLPMCPFGQCYSRVVHCSDLGLTSVPTNIPDTRMLDLQNNKIKEIKEND 120

QY 121 FKGLTSLGLILNNKLFKHPKAFLLTKKLRRLYLSHNSQLSETPLNPKSLAELRIHEN 180  
 Db 121 FKGLTSLGLILNNKLFKHPKAFLLTKKLRRLYLSHNSQLSETPLNPKSLAELRIHEN 180

QY 181 KYVKIKQKDTFKGMALHVLMSANPLDNNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPP 240  
 Db 181 KYVKIKQKDTFKGMALHVLMSANPLDNNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPP 240

QY 241 TLELHLIDYKNISTVELEDFRYKELQRLGLGNKKITDIENGSLANIPIRVREIHLNNKL 300  
 Db 241 TLELHLIDYKNISTVELEDFRYKELQRLGLGNKKITDIENGSLANIPIRVREIHLNNKL 300

QY 301 KKIPSGLPKYLQIIFLHNSIARVGVNDFCPTVPKMKSLYSALISLNNPVKYWEMQP 360  
 Db 301 KKIPSGLPKYLQIIFLHNSIARVGVNDFCPTVPKMKSLYSALISLNNPVKYWEMQP 360

QY 361 ATFRCVLSRMSVQLGNFCM 379  
 Db 361 ATFRCVLSRMSVQLGNFCM 379

RESULT 3  
 ABB95437  
 ID ABB95437 standard; Protein: 379 AA.  
 AC ABB95437;  
 XX  
 XX 19-JUL-2002 (first entry)  
 DE Human angiogenesis related protein PRO241 SEQ ID NO: 30.  
 KW Human: angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
 KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;  
 XX antiarteriosclerotic.  
 XX Homo sapiens.  
 OS

XX WO200208284-A2.  
 PN 31-JAN-2002.  
 XX  
 XX 09-JUL-2001; 2001WO-US21735.  
 XX 20-JUL-2000; 2000US-219556P.  
 PR 25-JUL-2000; 2000US-220624P.  
 PR 25-JUL-2000; 2000US-220664P.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 02-AUG-2000; 2000US-222695P.  
 PR 17-AUG-2000; 2000US-0643657.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 07-SEP-2000; 2000US-230978P.  
 PR 15-SEP-2000; 2000US-000000P.  
 PR 18-SEP-2000; 2000US-0664610.  
 PR 24-SEP-2000; 2000US-0665350.  
 PR 24-OCT-2000; 2000US-242922P.  
 PR 08-NOV-2000; 2000US-0709238.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 22-JAN-2001; 2001US-0767609.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0808689.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 30-MAY-2001; 2001US-0870574.  
 PR 30-MAY-2001; 2001WO-US17443.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 28-JUN-2001; 2001WO-US00000.  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA (BAKE/) BAKER K P.  
 PA (FERR/) FERRARA N.  
 PA (GERB/) GERBER H.  
 PA (GERK/) GERRITSEN M E.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GURN/) GURNEY A L.  
 PA (HILL/) HILLAN K J.  
 PA (MARS/) MARSTERS S A.  
 PA (PANJ/) PAN J.  
 PA (PAONI/) PAONI N F.  
 PA (STEP/) STEPHAN J F.  
 PA (WATA/) WATANABE C K.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 XX  
 XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KU, Marsters SA, Pan J, Paoni NF;  
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
 XX  
 XX WPI: 2002-171999/22.  
 DR N-PSDB; ABL95575.  
 XX  
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal -  
 XX

PS Claim 11; Fig 30; 567pp; English.

XX The present invention provides the protein and coding sequences of human

CC PRO proteins. These are useful for treating or diagnosing a

CC cardiovascular, endothelial or angiogenic disorder, including cardiac

CC hypertrophy, trauma, cancer, age-related macular degeneration,

CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,

CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour

CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound

CC healing. The present sequence is a PRO protein of the invention.

XX Sequence 379 AA;

SQ

Query Match 100.0%; Score 1992; DB 23; Length 379;

Best Local Similarity 100.0%; Pred. No. 4e-177;

Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFPTR 60

Db 1 MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFPTR 60

QY 61 PRSHFFPDLPMCPFGCQYSRVHSCDGLTSVPTNIPFTRMLDLQNNKIKEIKEND 120

Db 61 PRSHFFPDLPMCPFGCQYSRVHSCDGLTSVPTNIPFTRMLDLQNNKIKEIKEND 120

QY 121 FKGLTSLYGLILNNKLTTHPKAFLTKLRRLYLHSHNOLSEIPLNPKSLAELRIHEN 180

Db 121 FKGLTSLYGLILNNKLTTHPKAFLTKLRRLYLHSHNOLSEIPLNPKSLAELRIHEN 180

QY 161 KVKTKQDTFKGMALHVLNSANPLDNGIEPCAFEGVTVFHIRIAEAKLTSVPKGLPP 240

Db 161 KVKTKQDTFKGMALHVLNSANPLDNGIEPCAFEGVTVFHIRIAEAKLTSVPKGLPP 240

QY 241 TLLEHLHDYKISTVELEDFKRYELQRLGKNNKIITDIENGSLANIPRVREIHLNNKL 300

Db 241 TLLEHLHDYKISTVELEDFKRYELQRLGKNNKIITDIENGSLANIPRVREIHLNNKL 300

QY 301 KKIPSGLPKYLQIIFLHNSIARVGVNDFCPVTPKMKKSLYSASISLFPNNPKYWMQ 360

Db 301 KKIPSGLPKYLQIIFLHNSIARVGVNDFCPVTPKMKKSLYSASISLFPNNPKYWMQ 360

QY 361 ATFRCLVSRMSVQLGNFGM 379

Db 361 ATFRCLVSRMSVQLGNFGM 379

RESULT 4

ABB84831

ID ABB84831 standard; Protein; 379 AA.

XX ABB84831;

XX ABB84831;

DT 16-MAY-2002 (first entry)

DE Human PRO241 protein sequence SEQ ID NO:30.

DE Human: angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;

KW vulnerable; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;

KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;

KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;

KW age-related macular degeneration; arterial restenosis; angina;

KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;

KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;

KW wound healing; chromosome mapping; gene mapping.

XX Homo sapiens.

OS

XX WO200200690-A2.

XX

PD 03-JAN-2002.

XX

PF 20-JUN-2001; 2001WO-US19692.

XX

PR 23-JUN-2000; 2000US-213637P.

PR 20-JUL-2000; 2000US-219556P.

PR 25-JUL-2000; 2000US-220624P.

PR 25-JUL-2000; 2000US-220664P.

PR 28-JUL-2000; 2000WO-US20710.

PR 02-AUG-2000; 2000US-222695P.

PR 17-AUG-2000; 2000US-0643657.

PR 23-AUG-2000; 2000WO-US23522.

PR 24-AUG-2000; 2000WO-US23328.

PR 07-SEP-2000; 2000US-230978P.

PR 18-SEP-2000; 2000US-0664610.

PR 18-SEP-2000; 2000US-0665350.

PR 24-OCT-2000; 2000US-242922P.

PR 08-NOV-2000; 2000US-0709238.

PR 08-NOV-2000; 2000WO-US30952.

PR 10-NOV-2000; 2000WO-US30873.

PR 01-DEC-2000; 2000WO-US32678.

PR 20-DEC-2000; 2000US-0747259.

PR 20-DEC-2000; 2000WO-US34956.

PR 22-JAN-2001; 2001US-0767609.

PR 28-FEB-2001; 2001US-0796498.

PR 28-FEB-2001; 2001WO-US06520.

PR 01-MAR-2001; 2001WO-US06666.

PR 09-MAR-2001; 2001US-0802706.

PR 14-MAR-2001; 2001US-0808689.

PR 22-MAR-2001; 2001US-0816744.

PR 05-APR-2001; 2001US-0828366.

PR 10-MAY-2001; 2001US-0854208.

PR 10-MAY-2001; 2001US-0854280.

PR 25-MAY-2001; 2001US-0866028.

PR 25-MAY-2001; 2001US-0866034.

PR 30-MAY-2001; 2001WO-US17092.

PR 30-MAY-2001; 2001US-0870574.

PR 01-JUN-2001; 2001WO-US17443.

PR 01-JUN-2001; 2001WO-US17800.

XX (GETH ) GENENTECH INC.

PA Baker KP, Ferrara N, Gerber H, Gertsen ME, Goddard A;

PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;

PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX WPI: 2002-090516/12.

DR N-PSDB; ABL88086.

DR

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,

PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial

PT infarction), endothelial or angiogenic disorders in a mammal -

XX

PS Claim 11; Fig 30; 565pp; English.

XX

CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to

CC ABB85003. The PRO proteins and polynucleotides have cardiac, cytostatic,

CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic

CC activities, and can be used in gene therapy. The PRO polynucleotides,

CC proteins, agonists and antagonists are useful for treating or diagnosing

CC a cardiovascular, endothelial or angiogenic disorder in a mammal,

CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular

CC degeneration, atherosclerosis, hypertension, arterial restenosis,

CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,

CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver

CC carcinoma) and wound healing. The PRO polynucleotides have applications

CC in molecular biology, including use as hybridisation probes, and in

CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and

CC probes used in the exemplification of the present invention.

XX

SQ Sequence 379 AA;

Query Match 100.0%; Score 1992; DB 23; Length 379;

Best Local Similarity 100.0%; Pred. No. 4e-177;

Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFPTR 60





QY 241 TLELHLDYKISTVELEDFKRYELQRLGLGNKKITDIENGSLANIPRVREIHLNNKL 300  
 DB 235 TLELHLDYKISTVELEDFKRYELQRLGLGNKKITDIENGSLANIPRVREIHLNNKL 294  
 QY 301 KKPISGLPELKYLIIFLHNSIARVGVNDPCPTVPKMKKSLYSALSFLNPNKYWEMQP 360  
 DB 295 KKPISGLPELKYLIIFLHNSIARVGVNDPCPTVPKMKKSLYSALSFLNPNKYWEMQP 354  
 QY 361 ATFRVLSRMSVQLGNFG 378  
 DB 355 ATFRVLSRMSVQLGNVG 372

RESULT 8  
 AAM40351  
 ID AAM40351 standard; Protein: 344 AA.  
 XX  
 AC AAM40351;  
 DT 22-OCT-2001 (first entry)  
 XX Human polypeptide SEQ ID NO 3496.  
 DE  
 XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200153312-A1.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 26-DEC-2000; 2000WO-US34263.  
 XX  
 PR 21-JAN-2000; 2000US-0488725.  
 PR 25-APR-2000; 2000US-052317.  
 PR 09-JUL-2000; 2000US-0598042.  
 PR 19-JUL-2000; 2000US-0620312.  
 PR 03-AUG-2000; 2000US-0653450.  
 PR 14-SEP-2000; 2000US-0662191.  
 PR 19-OCT-2000; 2000US-0693036.  
 PR 29-NOV-2000; 2000US-0727344.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
 XX  
 DR WPI; 2001-442253/47.  
 DR N-PSDB; AAI59507.  
 XX  
 PT Novel nucleic acids and polypeptides, useful for treating disorders  
 PT such as central nervous system injuries -  
 XX  
 PS Example 6; SEQ ID NO 3496; 10078pp; English.  
 XX  
 CC The invention relates to human nucleic acids (AAI57798-AAI61369) and  
 CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,  
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localised neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: Immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemias and  
 CC C.N.S disorders.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification.  
 XX  
 SQ Sequence 344 AA;  
 Query Match 82.8%; Score 1649; DB 22; Length 344;  
 Best Local Similarity 97.5%; Pred. No. 3.3e-145;  
 Matches 316; Conservative 1; Mismatches 7; Indels 0; Gaps 0;  
 QY 56 FPTPREPRSHFFPDLFPMCPFGCCYCYRVVHCGSDGLTVPNTIPDTRMLDQNNKIKE 115  
 DB 21 FQESQEAIFFPDLFPMCPFGCCYCYRVVHCGSDGLTVPNTIPDTRMLDQNNKIKE 80  
 QY 116 IKENDEFGLTSLYGLILNNKKLTTHPKAFLTTKKLRLYLSHNSLSEIPLNPKSLAEL 175  
 DB 81 IKENDEFGLTSLYGLILNNKKLTTHPKAFLTTKKLRLYLSHNSLSEIPLNPKSLAEL 140  
 QY 176 RIHENKVKTKQDTFKGMNALHVLEMSANPLDNNNGIEPGAFEGVTVFHIRIAEAKLTSP 235  
 DB 141 RIHENKVKTKQDTFKGMNALHVLEMSANPLDNNNGIEPGAFEGVTVFHIRIAEAKLTSP 200  
 QY 236 KGLPPTLELHLDYKISTVELEDFKRYKELORLGLGNKKITDIENGSLANIPRVREIHL 295  
 DB 201 KGLPPTLELHLDYKISTVELEDFKRYKELORLGLGNKKITDIENGSLANIPRVREIHL 260  
 QY 296 ENNKLKIPSGLPPELKYLIIFLHNSIARVGVNDPCPTVPKMKKSLYSALSFLNPNKY 355  
 DB 261 ENNKLKIPSGLPPELKYLIIFLHNSIARVGVNDPCPTVPKMKKSLYSALSFLNPNKY 320  
 QY 356 WEMQATFRVLSRMSVQLGNFGM 379  
 DB 321 WEMQATFRVLSRMSVQLGNFGM 344

RESULT 9  
 ABG22569  
 ID ABG22569 standard; Protein: 352 AA.  
 XX  
 AC ABG22569;  
 DT 18-FEB-2002 (first entry)  
 XX Novel human diagnostic protein #22560.  
 DE  
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200175067-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US08631.  
 XX  
 PR 31-MAR-2000; 2000US-0540217.  
 PR 23-AUG-2000; 2000US-0649167.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YT;  
 XX  
 DR WPI; 2001-639362/73.  
 DR N-PSDB; AAS86756.  
 XX  
 PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity -  
 XX



3:





XX 02-JUN-1995; 95US-0458834.  
 XX 14-NOV-1991; 91US-0792192.  
 PR 17-NOV-1992; 92US-0978931.  
 PR 08-SEP-1994; 94US-0303238.  
 PR 28-JUN-1988; 88US-0212702.  
 PR 22-JAN-1990; 90US-0467888.  
 PR 13-MAY-1992; 92US-0882345.  
 XX (BURN-) BURNHAM INST.  
 PA Ruoslahti EI, Yamaguchi Y;  
 PI WPI; 2001-610491/70.  
 XX Use of decorin or biglycan polypeptide for inhibiting TGF-beta activity  
 PT in the treatment of dermal wounds and cancer -  
 PS Example 7; Fig 11; 40pp; English.  
 XX The invention relates to the inhibition of transforming growth  
 CC factor-beta (TGF-beta) activity involving contacting TGF-beta with a  
 CC purified polypeptide comprising leucine-rich amino acid sequence of a  
 CC member of decorin superfamily of mammalian proteoglycans. The following  
 CC activities can be attributed to the polypeptide of the invention:  
 CC cytostatic, nephrotropic, antirheumatic, antiarthritic, vasotropic,  
 CC antiarteriosclerotic, hepatotropic, cardiant, dermatological and  
 CC vulnerary. Polypeptides of the invention act as transforming growth  
 CC factor-beta (TGF-beta) binder. The polypeptides of the invention can be  
 CC used for treating a pathology, particularly proliferative pathology  
 CC caused by a transforming growth factor-beta (TGF-beta) regulated  
 CC activity such as cancer; particularly fibrotic cancer, fibrotic  
 CC disease, glomerulonephritis, rheumatoid arthritis, arteriosclerosis,  
 CC adult respiratory distress syndrome, cirrhosis of liver, fibrosis of  
 CC lungs, post-myocardial infarction, cardiac fibrosis, post-angioplasty  
 CC restenosis, renal interstitial fibrosis and certain dermal fibrotic  
 CC conditions such as keloids and scarring resulting from burn injuries;  
 CC other invasive skin injuries and reconstructive surgery. The wounds  
 CC treated with the polypeptide, particularly decorin exhibit no detectable  
 CC scarring, and are histologically normal. The current sequence represents  
 CC human biglycan.  
 XX Sequence 368 AA;  
 SQ  
 Query Match 51.3%; Score 1021; DB 22; Length 368;  
 Best Local Similarity 52.4%; Pred. No. 1.3e-86;  
 Matches 197; Conservative 64; Mismatches 95; Indels 20; Gaps 3;  
 QY 6 LLLFLALCSAKPF-----FSPSHIALKNMMLKDMEDTDDDDDDDDDDDDSLFPTREP 61  
 Db 7 LVSLALSQLPFEQGFWDFTLDGPFMMNDEASGADTSGVLDPD-----SVTPYTS- 60  
 QY 62 RSHFFPDLFPMCPFGCCYSRVVHCHSDGLTSTPTNIPEDTMRDLQNNKIKEIKENDF 121  
 Db 61 -----AMCPFGCHLRVYVQCSDLGLKSPKETSPTDTLLDQNNDISLRKDDF 110  
 QY 122 KGLTSLYGLIILNNKTKIHPKAFITTKKRLRYLSHNLSEIPLNLPKSLAELRIHENK 181  
 Db 111 KGLQHLVALVLVNNKISKIHEKAFSPLRNVQKLYISKHNLVEIPLNLPSSILVELRIHDNR 170  
 QY 182 VKKIQKDTFKGMNALHVLMSANPLDNGIEPGAFEGVTVFHRTAEAKLTSPKGLPPT 241  
 Db 171 IRKVPNGVFSGLURNMNCIENGNGPFGAFDGLKLYLRISAEAKLTGIPRDPET 230  
 QY 242 LLEHLNDYKISTVELEDFKRYKELQRLGLGNKTKITDIENGSLANIPRVREIHLNKKLK 301  
 Db 231 LNELHLDNKKIQAEIEDLLRYSKLYRLGLGHQNRIMLENGSLFPLTLRELHLDNKKLA 290  
 QY 302 KIPSGLPKLYLQITFLHSNSTARVGVNDFCTVPKMKKSLYSATSLFPNNPVKYWEQPA 361  
 Db 291 RVPSPGLPDLKLQVYLYHSNNITKGVNDFCPMGFGVKRAYNGISLFPNNPVYWEQPA 350

QY 362 TFRCVLSRMSVQLGNF 377  
 Db 351 TFRCVTDRLAIQFGNY 366  
 RESULT 15  
 AAR05159  
 ID AAR05159 standard; protein; 368 AA.  
 XX  
 AC AAR05159;  
 XX  
 DT 17-DEC-2001 (updated)  
 DT 09-OCT-1990 (first entry)  
 XX  
 DE Sequence of human bone proteoglycan I (biglycan).  
 XX Osteoporosis; rheumatoid arthritis; Paget's disease;  
 KW atherosclerosis; periodontal; human bone matrix; proteoglycan.  
 XX Homo sapiens.  
 XX USN7432044-N.  
 PN 17-APR-1990.  
 PD 03-NOV-1989; 89US-0432044.  
 XX 03-NOV-1989; 89US-0432044.  
 PR (USSH ) NAT INST OF HEALTH.  
 PA Termino J;  
 PI WPI; 1990-178641/23.  
 DR N-PSDB; AAQ04490.  
 XX Human bone matrix DNA and proteins -  
 PT used in detection, diagnosis and treatment involving skeletal  
 PT and/or connective tissue disease states.  
 XX Disclosure; ; p; English.  
 XX Probes and Abs raised to the proteins can be used to determine  
 CC their levels useful in diagnosis of associated connective tissue  
 CC diseases states such as osteoporosis, osteoarthritis, arthritis,  
 CC Paget's disease, atherosclerosis and periodontal disease.  
 CC Proteins may also be used to induce or block biological function.  
 CC (Note: Revised entry submitted to correct the patent number format of  
 CC US Government-owned NTIS applications to prevent clashes with ongoing US  
 CC granted patent numbers. For further information please visit the Derwent  
 CC web site at [www.derwent.com/dwpl/updates/ntis\\_us.html](http://www.derwent.com/dwpl/updates/ntis_us.html).)  
 XX  
 SQ Sequence 368 AA;  
 Query Match 51.2%; Score 1020; DB 11; Length 368;  
 Best Local Similarity 52.1%; Pred. No. 1.6e-86;  
 Matches 196; Conservative 66; Mismatches 94; Indels 20; Gaps 3;  
 QY 6 LLLFLALCSAKPF-----FSPSHIALKNMMLKDMEDTDDDDDDDDDDDDSLFPTREP 61  
 Db 7 LVSLALSQLPFEQGFWDFTLDGPFMMNDEASGADTSGVLDPD-----SVTPYTS- 60  
 QY 62 RSHFFPDLFPMCPFGCCYSRVVHCHSDGLTSTPTNIPEDTMRDLQNNKIKEIKENDF 121  
 Db 61 -----AMCPFGCHLRVYVQCSDLGLKSPKETSPTDTLLDQNNDISLRKDDF 110  
 QY 122 KGLTSLYGLIILNNKTKIHPKAFITTKKRLRYLSHNLSEIPLNLPKSLAELRIHENK 181  
 Db 111 KGLQHLVALVLVNNKISKIHEKAFSPLRNVQKLYISKHNLVEIPLNLPSSILVELRIHDNR 170  
 QY 182 VKKIQKDTFKGMNALHVLMSANPLDNGIEPGAFEGVTVFHRTAEAKLTSPKGLPPT 241  
 Db 171 IRKVPNGVFSGLURNMNCIENGNGPFGAFDGLKLYLRISAEAKLTGIPRDPET 230



CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localised neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: Immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemias and  
 CC C.N.S disorders.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification.

XX Sequence 197 AA;  
 CC Query Match 50.6%; Score 1007; DB 22; Length 197;  
 CC Best Local Similarity 99.0%; Pred. No. 1.1e-85;  
 CC Matches 191; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 MKEYVLLFLALCSAKPFSPSHIALKNMMLKDMEDT---DDDDDDDDDDDDDDNSLPPT 58  
 Db 3 MKEYVLLFLALCSAKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDNSLPPT 62  
 QY 59 REPRSHFFPDLPMCPFCGCQYSRVVHCSGLTSVPTNIPDTRMLDLQNNKIKE 118  
 Db 63 REPRSHFFPDLPMCPFCGCQYSRVVHCSGLTSVPTNIPDTRMLDLQNNKIKE 122  
 QY 119 NDFKGLTSLYGLTLNNKLTTHPKAFLTKLRRLYLSHNLSEIPLNPKSLAELRH 178  
 Db 123 NDFKGLTSLYGLTLNNKLTTHPKAFLTKLRRLYLSHNLSEIPLNPKSLAELRH 182  
 QY 179 ENVKKIQKDTFK 191  
 Db 183 ENVKKIQKDTFK 195

RESULT 19  
 AAY57079  
 ID AAY57079 standard; protein; 359 AA.  
 XX AC AAY57079;  
 XX DT 28-FEB-2000 (first entry)  
 XX DE Human decorin amino acid sequence.  
 XX Neglected target tissue antigen; NNTA; autoimmunity; autoimmune response;  
 KW immunotherapeutic agent; insulin dependent diabetes mellitus;  
 KW multiple sclerosis; autoimmune thyroiditis; rheumatoid arthritis;  
 KW uveoretinitis; inflammatory response.  
 XX OS Homo sapiens.  
 XX WO9956763-A1.  
 XX PD 11-NOV-1999.  
 XX PF 07-MAY-1999; 99WO-US10250.  
 XX PR 07-MAY-1998; 98US-0084636.  
 XX PA (REGC ) UNIV CALIFORNIA.  
 XX Kaufman DL, Tian J, Olcott A;  
 XX WPI: 2000-052905/04.  
 XX Administration of neglected target tissue antigens to modulate immune  
 PT responses -  
 XX Disclosure; Page 26; 79pp; English.

CC Amino acid sequences AAY57063-Y57091 are examples of neglected target  
 CC tissue antigens NNTAs. NNTAs are antigens (whole antigens or fragments)  
 CC not involved in autoimmunity. These peptides and proteins are used in  
 CC the method of the invention which involves administering an NNTA as an  
 CC antigen based immunotherapeutic agent, to a host afflicted with an  
 CC autoimmune response associated with an autoimmune disease. The  
 CC immunotherapeutic agent is used to treat autoimmune diseases such as  
 CC insulin dependent diabetes mellitus, multiple sclerosis, autoimmune  
 CC thyroiditis, uveoretinitis, rheumatoid arthritis or abnormal  
 CC inflammatory immune responses. The NNTA induces regulatory tolerance by  
 CC elicitation of regulatory T cells among T cells recognizing the NNTA but  
 CC not participating in the immune response. The NNTA are capable of  
 CC recognition by substantial populations of uncommitted T cells which can  
 CC be primed, or biased, towards regulatory responses to provide effective  
 CC treatment. The NNTA are effective in regulating undesirable immune  
 CC responses even when target determinants used as agents promoting  
 CC tolerance agents have failed to induce an effective regulatory T cell  
 CC response. NNTAs as agents promoting tolerance are anticipated to be safer  
 CC than use of target determinants.

XX Sequence 359 AA;  
 CC Query Match 48.4%; Score 963.5; DB 21; Length 359;  
 CC Best Local Similarity 50.4%; Pred. No. 2.9e-81;  
 CC Matches 191; Conservative 65; Mismatches 100; Indels 23; Gaps 4;  
 QY 1 MKEYVLLFLALCS-AKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLPPT 59  
 Db 1 MKATITILLALQVSWAGPF--QORGLPDFMLEDEASGIGPEVDDR----- 45  
 QY 60 EPRSHFFPDLPMCPFCGCQYSRVVHCSGLTSVPTNIPDTRMLDLQNNKIKE 119  
 Db 46 -----PEPSLGPVCPFRQCCHLRVVQCDLGLDKVPKDLPPDTLLDLQNNKITE 99  
 QY 120 DFKGLTSLYGLTLNNKLTTHPKAFLTKLRRLYLSHNLSEIPLNPKSLAELRH 179  
 Db 100 DFKNLKHLALILVNNKISKVSPGAFPLVKLRILYLSKNLKEPKMPTLQELRAH 159  
 QY 180 NVKKIQKDTFKGMNALHLEMSANPLDNGIEGAFGV-TVPHIRTAELKSLVPKGL 238  
 Db 160 NEITKVRKVTENGMLNQMIVIELGTNPLKSSGIEGAFGVGKLSYIRIADTNISIPGL 219  
 QY 239 PPTLELHLDYNNKISTVELEDFKRYKELQRLGLGNKLTIDENGSLANIPVRETHLENN 298  
 Db 220 PPSLTELHLDGNKISRVDAAASLKGLNLAELGSEISAVDNGSLANTPHRLHLDNN 279  
 QY 299 KLKIPSGELPELKYLIIFLHNSIARVGVNDFCTVPKMKKSLYSALSLENNPVYWE 358  
 Db 280 KLTRVPGGLAEHKYIQVYVYLNHNINISVVGSSDFCPGHTKKASVGSVLSFNPVYWE 339  
 QY 359 QPATERCVLSRMSVOLGNF 377  
 Db 340 QPATERCVLSRMSVOLGNF 358

RESULT 19  
 AAG78511  
 ID AAG78511 standard; protein; 359 AA.  
 XX AC AAG78511;  
 XX DT 29-JAN-2002 (first entry)  
 XX DE Human decorin amino acid sequence.  
 XX Fibromodulin; Decorin; Biglycan; Proteoglycan; Extracellular matrix;  
 KW TGF-beta; Transforming growth factor-beta; Burn; Wound; Cytostatic;  
 KW Nephrotropic; Antirheumatic; Antiarthritic; Vasotropic; Vulnerary  
 KW Antiartherosclerotic; Hepatotropic; Cardiant; Dermatological;  
 KW glomerulonephritis; Rheumatoid arthritis; Arteriosclerosis;  
 KW Adult respiratory distress syndrome; Cirrhosis; Cancer; Fibrotic.  
 XX OS Homo sapiens.



PR 14-AUG-2000; 2000US-0225759.  
 PR 18-AUG-2000; 2000US-0226279.  
 PR 22-AUG-2000; 2000US-0226681.  
 PR 22-AUG-2000; 2000US-0226868.  
 PR 23-AUG-2000; 2000US-0227182.  
 PR 30-AUG-2000; 2000US-0227009.  
 PR 01-SEP-2000; 2000US-0228924.  
 PR 01-SEP-2000; 2000US-0229287.  
 PR 01-SEP-2000; 2000US-0229343.  
 PR 01-SEP-2000; 2000US-0229344.  
 PR 01-SEP-2000; 2000US-0229345.  
 PR 05-SEP-2000; 2000US-0229509.  
 PR 05-SEP-2000; 2000US-0229513.  
 PR 06-SEP-2000; 2000US-0230437.  
 PR 06-SEP-2000; 2000US-0230438.  
 PR 08-SEP-2000; 2000US-0231242.  
 PR 08-SEP-2000; 2000US-0231243.  
 PR 08-SEP-2000; 2000US-0231244.  
 PR 08-SEP-2000; 2000US-0231413.  
 PR 08-SEP-2000; 2000US-0231414.  
 PR 08-SEP-2000; 2000US-0232080.  
 PR 08-SEP-2000; 2000US-0232081.  
 PR 12-SEP-2000; 2000US-0231968.  
 PR 14-SEP-2000; 2000US-0232397.  
 PR 14-SEP-2000; 2000US-0232398.  
 PR 14-SEP-2000; 2000US-0232399.  
 PR 14-SEP-2000; 2000US-0232400.  
 PR 14-SEP-2000; 2000US-0232401.  
 PR 14-SEP-2000; 2000US-0233063.  
 PR 14-SEP-2000; 2000US-0233064.  
 PR 14-SEP-2000; 2000US-0233065.  
 PR 21-SEP-2000; 2000US-0234223.  
 PR 21-SEP-2000; 2000US-0234274.  
 PR 25-SEP-2000; 2000US-0234997.  
 PR 25-SEP-2000; 2000US-0234998.  
 PR 26-SEP-2000; 2000US-0235484.  
 PR 27-SEP-2000; 2000US-0235834.  
 PR 27-SEP-2000; 2000US-0235836.  
 PR 29-SEP-2000; 2000US-0236327.  
 PR 29-SEP-2000; 2000US-0236367.  
 PR 29-SEP-2000; 2000US-0236368.  
 PR 29-SEP-2000; 2000US-0236369.  
 PR 29-SEP-2000; 2000US-0236370.  
 PR 02-OCT-2000; 2000US-0236802.  
 PR 02-OCT-2000; 2000US-0237037.  
 PR 02-OCT-2000; 2000US-0237038.  
 PR 02-OCT-2000; 2000US-0237039.  
 PR 02-OCT-2000; 2000US-0237040.  
 PR 13-OCT-2000; 2000US-0239935.  
 PR 13-OCT-2000; 2000US-0239937.  
 PR 20-OCT-2000; 2000US-0240960.  
 PR 20-OCT-2000; 2000US-0241221.  
 PR 20-OCT-2000; 2000US-0241785.  
 PR 20-OCT-2000; 2000US-0241786.  
 PR 20-OCT-2000; 2000US-0241787.  
 PR 20-OCT-2000; 2000US-0241808.  
 PR 20-OCT-2000; 2000US-0241809.  
 PR 20-OCT-2000; 2000US-0241826.  
 PR 01-NOV-2000; 2000US-0244617.  
 PR 08-NOV-2000; 2000US-0246474.  
 PR 08-NOV-2000; 2000US-0246475.  
 PR 08-NOV-2000; 2000US-0246476.  
 PR 08-NOV-2000; 2000US-0246477.  
 PR 08-NOV-2000; 2000US-0246478.  
 PR 08-NOV-2000; 2000US-0246523.  
 PR 08-NOV-2000; 2000US-0246524.  
 PR 08-NOV-2000; 2000US-0246525.  
 PR 08-NOV-2000; 2000US-0246526.  
 PR 08-NOV-2000; 2000US-0246527.  
 PR 08-NOV-2000; 2000US-0246528.  
 PR 08-NOV-2000; 2000US-0246532.  
 PR 08-NOV-2000; 2000US-0246609.  
 PR 08-NOV-2000; 2000US-0246610.

PR 08-NOV-2000; 2000US-0246611.  
 PR 08-NOV-2000; 2000US-0246613.  
 PR 17-NOV-2000; 2000US-0249207.  
 PR 17-NOV-2000; 2000US-0249208.  
 PR 17-NOV-2000; 2000US-0249209.  
 PR 17-NOV-2000; 2000US-0249210.  
 PR 17-NOV-2000; 2000US-0249211.  
 PR 17-NOV-2000; 2000US-0249212.  
 PR 17-NOV-2000; 2000US-0249213.  
 PR 17-NOV-2000; 2000US-0249214.  
 PR 17-NOV-2000; 2000US-0249215.  
 PR 17-NOV-2000; 2000US-0249216.  
 PR 17-NOV-2000; 2000US-0249217.  
 PR 17-NOV-2000; 2000US-0249218.  
 PR 17-NOV-2000; 2000US-0249244.  
 PR 17-NOV-2000; 2000US-0249245.  
 PR 17-NOV-2000; 2000US-0249264.  
 PR 17-NOV-2000; 2000US-0249265.  
 PR 17-NOV-2000; 2000US-0249297.  
 PR 17-NOV-2000; 2000US-0249299.  
 PR 17-NOV-2000; 2000US-0249300.  
 PR 01-DEC-2000; 2000US-0250160.  
 PR 01-DEC-2000; 2000US-0250391.  
 PR 05-DEC-2000; 2000US-0251030.  
 PR 05-DEC-2000; 2000US-0251988.  
 PR 05-DEC-2000; 2000US-0256719.  
 PR 06-DEC-2000; 2000US-0251479.  
 PR 08-DEC-2000; 2000US-0251856.  
 PR 08-DEC-2000; 2000US-0251868.  
 PR 08-DEC-2000; 2000US-0251869.  
 PR 08-DEC-2000; 2000US-0251989.  
 PR 08-DEC-2000; 2000US-0251990.  
 PR 11-DEC-2000; 2000US-0254097.  
 PR 05-JAN-2001; 2001US-0259678.  
 XX  
 (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 Rosen CA, Barash SC, Ruben SM;  
 WPI; 2001-581633/65.  
 DR N-PSDB; ABK43616.  
 XX  
 New Isolated nucleic acid encoding a protein for diagnosing,  
 PT preventing, treating or ameliorating medical conditions and used as  
 PT food additives or preservatives -  
 XX  
 Claim 9; SEQ ID No 804; 837pp; English.  
 PS  
 XX  
 The invention describes an isolated nucleic acid molecule (I) encoding a  
 CC novel central nervous system protein. (I) and polypeptides (III) encoded  
 CC by (I), are used to treat a medical conditions and in diagnosis of a  
 CC pathological condition. Disorders which are diagnosed or treated include  
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative  
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders  
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,  
 CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and  
 CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses  
 CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders  
 CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,  
 CC adenocarcinomas and irritable bowel syndrome, reproductive system  
 CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes  
 CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.  
 CC leukemia, disorders involving neovascularisation e.g. malignancies,  
 CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.  
 CC acute kidney failure and blood related disorders e.g. myocardial  
 CC infarction. The polypeptides can also be used to aid wound healing and  
 CC epithelial cell proliferation, to prevent skin aging due to sunburn, to  
 CC maintain organs before transplantation, for supporting cell culture of  
 CC primary tissues, to regenerate tissues and in chemotaxis. The  
 CC polypeptides can also be used as a food additive or preservative to  
 CC increase or decrease storage capabilities, fat content, lipid, protein,  
 CC

Query Match

48.4%; Score 963.5; DB 22; Length 360;





ID AAY84539 standard; Protein; 1388 AA.  
 XX AAY84539;  
 XX 25-JUL-2000 (first entry)  
 XX Amino acid sequence of a chimeric collagen 1 (alpha1)/decorin protein.  
 XX  
 XX Extracellular matrix protein; self aggregation; hydroxylated proline;  
 KW trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production;  
 KW collagen; fibrinogen; fibronectin; post translational hydroxylation;  
 KW decorin; chimera.  
 XX  
 OS Chimeric - Homo sapiens.  
 OS Chimeric - Unidentified.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 87 /note= "Gly encoded by GCG"  
 FT Misc-difference 305 /note= "Glu encoded by CAA"  
 FT Misc-difference 363 /note= "Gly encoded by CGT"  
 FT Misc-difference 378 /note= "Glu encoded by GGT"  
 FT Misc-difference 429 /note= "Gly encoded by CGA"  
 FT Misc-difference 444 /note= "Gly encoded by GCG"  
 FT Misc-difference 543 /note= "Gly encoded by GCC"  
 FT Misc-difference 546 /note= "Gly encoded by GCT"  
 FT Misc-difference 606 /note= "Gly encoded by GAC"  
 FT Misc-difference 702 /note= "Gly encoded by CGT"  
 FT Misc-difference 815 /note= "Pro encoded by CTT"  
 FT Misc-difference 858 /note= "Gly encoded by GCT"  
 FT Misc-difference 1066 /note= "Gly encoded by GCC"  
 XX  
 XX EF992586-A2.  
 XX  
 XX 12-APR-2000.  
 XX  
 XX 07-OCT-1999; 99EP-0119184.  
 XX  
 XX 09-OCT-1998; 98US-0169768.  
 XX  
 XX (USSU ) US SURGICAL CORP.  
 XX  
 XX Gruskin EA, Buechter DD, Zhang G, Connolly K;  
 XX WPI; 2000-259138/23.  
 XX N-PSDB; AAA12499.  
 XX  
 XX Production of extracellular matrix proteins containing  
 FT 4-trans-hydroxyproline results in native self aggregating proteins,  
 FT useful on medical implants -  
 XX  
 XX Claim 25; Fig 17A-B; 260pp; English.  
 XX  
 XX The specification describes a method for producing an extracellular  
 CC matrix protein or its fragment. The extracellular matrix protein is  
 CC capable of self aggregating in a cell which does not ordinarily  
 CC hydroxylated prolines. The method comprises optimising a nucleic acid  
 CC sequence for expression in the cell by substitution of codons preferred  
 CC by that cell for naturally occurring codons not preferred by the cell;  
 CC incorporating the nucleic acid sequence into the cell; and contacting  
 CC the cell with a hypertonic growth medium containing at least one amino

CC acid, selected from the group consisting of trans-4-hydroxyproline and  
 CC 3-hydroxyproline to allow at least one of the amino acids to be  
 CC assimilated into the cell and incorporated into the extracellular matrix  
 CC protein. The method may be used to make host cells assimilate and  
 CC incorporate trans-4-hydroxyproline into proteins. This is especially  
 CC useful in the recombinant production of proteins such as collagen,  
 CC fibrinogen and fibronectin whose ability to self aggregate and produce  
 CC functional proteins depends on the post translational hydroxylation of  
 CC proline. The method is also useful in studying the structure and function  
 CC of polypeptides which do not normally contain trans-4-hydroxyproline.  
 CC The present sequence represents a chimeric collagen 1 (alpha1)/decorin  
 CC protein, which may be produced using the method of the invention.  
 XX  
 XX  
 SQ Sequence 1388 AA;  
 Query Match 47.5%; Score 947; DB 21; Length 1388;  
 Best Local Similarity 54.1%; Pred. No. 6.6e-79;  
 Matches 178; Conservative 62; Mismatches 87; Indels 2; Gaps 2;  
 QY 50 DDNSLFTTREPFRSHFFDFPFMCFCQCYSRVHVCSDGLGTSVPTNIPDFTRMLDLQ 109  
 DB 1060 DEASGIGP-EVPDDRDFEPLSLGVPVCFRCQCHLRVVCQSDGLGDKVPKDLPTLLDLQ 1118  
 QY 110 NKKIKENDEKGLTSLYGLILANNKLTKTTPKAFLTTKLRLRLYLSHNOLSEIPNL 169  
 DB 1119 NKKITTEIKDGFKNLKNLHALILVNNKISKVSPGAFPLVKLERLYLSKNOLKELPEKMP 1178  
 QY 170 KSLAELRIHENKVKKIQDKTFGMNALHVLMSANPLDNNGIEPGAFRGV-TVFHRIAE 228  
 DB 1179 KTLQELRAHENEITKRVKVTENGNGMIVIELGTNPLKSSGIENGAFOMKKLSYRIAD 1238  
 QY 229 AKLTSVPKGLPPTLLEHLHDYNNKISTVELEDFKRYKELQRLGNNKLTIDENGLANIP 288  
 DB 1239 TNITSIPOGLPPLTELHLDGNGKISRVDAAALKGLNNLAKLGLSFNSISAYDNGSLANTP 1298  
 QY 289 RYREIHLNENKLTPTSGLPKLYLQIIFLHNSNLTARVGVNDFCPTVPKMKKSLYSATSL 348  
 DB 1299 HLRELHLDNNKLTVPGGLAHEHYIQVYLHNNISVVGSSDFCPCPPGHNTKKASYSGVSL 1358  
 QY 349 FNNPVKYMOPATPCVLSRMSVOLGNF 377  
 DB 1359 FSNPVQYWEIQPSTFRFCVVRSAIQGNV 1387  
 RESULT 25  
 AAR05160  
 ID AAR05160 standard; protein; 353 AA.  
 XX  
 AC AAR05160;  
 XX  
 DT 17-DEC-2001 (updated)  
 DT 09-OCT-1990 (first entry)  
 XX  
 XX Sequence of human bone proteoglycan II (decorin).  
 DE  
 XX Osteoporosis; rheumatoid arthritis; Paget's disease;  
 KW atherosclerosis; periodontal; human bone matrix; proteoglycan.  
 XX  
 OS Homo sapiens.  
 XX  
 PN USN7432044-N.  
 XX  
 PD 17-APR-1990.  
 XX  
 PF 03-NOV-1989; 89US-0432044.  
 XX  
 PR 03-NOV-1989; 89US-0432044.  
 XX (USSH ) NAT INST OF HEALTH.  
 XX  
 PI Termino J;  
 XX  
 XX WPI; 1990-178641/23.



DR N-PSDB; AAQ0491.  
 XX Human bone matrix DNA and proteins -  
 PT used in detection, diagnosis and treatment involving skeletal  
 PT and/or connective tissue disease states.  
 XX Disclosure; ; p; English.  
 XX Probes and Abs raised to the proteins can be used to determine  
 CC their levels useful in diagnosis of associated connective tissue  
 CC diseases states such as osteoporosis, osteo/rheumatoid arthritis,  
 CC Paget's disease, artherosclerosis and periodontal disease.  
 CC Proteins may also be used to induce or block biological function.  
 CC (Note: Revised entry submitted to correct the patent number format of  
 CC US Government-owned NTIS applications to prevent clashes with ongoing US  
 CC granted patent numbers. For further information please visit the Derwent  
 CC web site at [www.derwent.com/dwpi/updates/ntis-us.html](http://www.derwent.com/dwpi/updates/ntis-us.html).)  
 XX SQ Sequence 353 AA;  
 Query Match 45.5%; Score 907; DB 11; Length 353;  
 Best Local Similarity 49.1%; Pred. No. 5.2e-76;  
 Matches 183; Conservative 61; Mismatches 107; Indels 22; Gaps 3;  
 QY 6 LLLFLALGSAKPPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDSLPPTREPRSHF 65  
 Db 1 LLLLAQVSWAGP---QORGLDFMLEDEASGIGPEVDDRD----- 39  
 QY 66 PFDLPFCPCGCGCYSRVHCSDGLTSTVNTNIPFDTMLDLQNNKIKEIKENDFKGLT 125  
 Db 40 FEPGLGVPFCPCGCHLRVQCSLDGLDKVPKDLPPDDTLLDLQNNKITEIKDGDENLK 99  
 QY 126 SLYGILLNNKLTAKHPKAFITTKLRRLYLHNLQSLSEIPLNLPKSLAELRIHENKVKKI 185  
 Db 100 NLHAILVNNKISKVSPGAFPLVKLERLYLSKNQKELPEKMPKTLQELRAHENEITKY 159  
 QY 186 QKDTFKGNALHVLMSANPLDNGNGIEGAFEGV-TVFHRIAEAKLTSPKGLPPTLLE 244  
 Db 160 RKTFTENGLNQIVIELGTNPLKSSGIENGAFQGMKLSYIRIATNTIKRVKVTFNGLTE 219  
 QY 245 LHLNYKISTVELEDFKRYKELQRLGLGNKKTIDENGSLANIPRVRIHLENNKLLKIP 304  
 Db 220 LHLNKGKISRDAASLKLNNLAKLGLSFNSISAVDNGSLANTPHLRELHLDNNKLRVP 279  
 QY 305 SGLPELKYLOIFLHNSIARVGNDECPYTPKMKLSYSAISLFPNPKYWEQWQATER 364  
 Db 280 GGLAEHKYIQVYLLHNNNISVVGSSDFCPGPHNTKASYSVGLSFSPVQYWEIQPSTFR 339  
 QY 365 CVLSRMSVOLGNF 377  
 Db 340 CVYVRSATQLGNY 352  
 RESULT 26  
 AAR42267  
 ID AAR42267 standard; Protein; 305 AA.  
 XX  
 AC AAR42267;  
 XX  
 DT 28-APR-1994 (first entry)  
 XX  
 DE Decorin sequence PT-78 (N-terminal to half C-terminal).  
 XX  
 KW leucine-rich repeat; proteoglycan; cell regulatory factor; MBP;  
 KW fusion protein; maltose binding protein; tumour growth; inhibition;  
 KW decorin; PG-II; PG-40; transforming growth factor-beta; TGF-beta.  
 XX  
 PN W09320202-A.  
 XX  
 PD 14-OCT-1993.  
 XX  
 PF 02-APR-1993; 93WO-US03171.  
 XX  
 PP

PR 03-APR-1992; 92US-0865652.  
 XX  
 PA (LJOL-) LA JOLLA CANCER RES FOUND.  
 XX  
 PI Cardenas J, Craig W, Mullen DG, Pierschbacher MD;  
 PI Ruoslahti EI;  
 XX  
 XX WPI: 1993-336910/42.  
 DR N-PSDB; AAQ50053.  
 XX  
 XX Active fragments of protein esp. decorin - with cell regulatory  
 PT factor domain, useful for inhibiting cell regulatory factor  
 PT activity  
 XX  
 PS Claim 10; Page 49-50; 77pp; English.  
 XX  
 CC Active fragments of decorin (full-length coding sequence AAQ50046)  
 CC were generated by PCR and fused to Maltose Binding Protein. The  
 CC resulting fusion proteins were useful for inhibiting the activity of  
 CC a cell regulatory factor, esp. TGF-beta, and hence for treating  
 CC conditions associated with over-activity of the growth factor such  
 CC as certain tumours.  
 XX  
 SQ Sequence 305 AA;  
 Query Match 42.5%; Score 847; DB 14; Length 305;  
 Best Local Similarity 53.3%; Pred. No. 1.7e-70;  
 Matches 162; Conservative 56; Mismatches 84; Indels 2; Gaps 2;  
 QY 50 DEINSFLPTREPRSHFPELFPFCGCGCYSRVHCSDGLTSTVNTNIPDTRMLDQ 109  
 Db 3 DEASGIGP-EVDDRDPEPSLGPVCFRCOCHLRVQCSLDGLDKVPKDLPPDPTLLDQ 61  
 QY 110 NNKIKEIKENDFKGLTSLYGLIILNNKLTAKHPKAFITTKLRRLYLHNLQSLSEIPLNLP 169  
 Db 62 NNKITEIKDGDENLKNNLHAILVNNKISKVSPGAFPLVKLERLYLSKNQKELPEKMP 121  
 QY 170 KSLAELRIHENKVKTKQDFTKGMNHALHVLMSANPLDNGNGIEGAFEGV-TVFHRIAE 228  
 Db 122 KTLQELRAHENEITKYKRVKVTFNGLNQIVIELGTNPLKSSGIENGAFQGMKLSYIRIAD 181  
 QY 229 AKLTSPKGLPPTLLEHLDYNNKISVLEDFKRYKELQRLGLGNKKTIDENGSLANTP 288  
 Db 182 TNITSIPQGLPSPTEHLHLDGNKISRDAASLKLNNLAKLGLSFNSISAVDNGSLANTP 241  
 QY 289 RVREIHLNENKLLKIPSGLPPELKYLOIFLHNSIARVGNDECPYTPKMKLSYSAISL 348  
 Db 242 HLRELHLDNNKLRVPGLAEHKYIQVYLLHNNNISVVGSSDFCPGPHNTKASYSVGL 301  
 QY 349 FNNP 352  
 Db 302 FSNP 305  
 RESULT 27  
 AAU30348  
 ID AAU30348 standard; Protein; 423 AA.  
 XX  
 AC AAU30348;  
 XX  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE Novel human secreted protein #839.  
 XX  
 KW Human; vaccination; gene therapy; nutritional supplement;  
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;  
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200179449-A2.  
 XX  
 PP 25-OCT-2001.

XX PF 16-APR-2001; 2001WO-US08656.  
 XX PR 18-APR-2000; 2000US-0552929.  
 XX PR 26-JAN-2001; 2001US-0770160.  
 XX PA (HYSE-) HYSEQ INC.  
 XX PI Tang YT, Liu C, Drmanac RT;  
 XX PI WPI; 2001-611725/70.  
 XX PT Nucleic acids encoding a range of human polypeptides, useful in genetic  
 XX PT vaccination, testing and therapy -  
 XX PS Claim 20; Page 281; 765pp; English.  
 XX CC The invention relates to novel human secreted polypeptides. The  
 CC polypeptides and antibodies to the polypeptides are useful for  
 CC determining the presence of or predisposition to a disease associated  
 CC with altered levels of polypeptide. The polypeptides are also useful for  
 CC identifying agents (agonists and antagonists) that bind to them. Cells  
 CC expressing the proteins are useful for identifying a therapeutic agent  
 CC for use in treatment of a pathology related to aberrant expression or  
 CC physiological interactions of the polypeptide. Vectors comprising  
 CC the nucleic acids encoding the polypeptides and cells genetically  
 CC engineered to express them are also useful for producing the proteins.  
 CC The proteins are useful in genetic vaccination, testing and  
 CC therapy, and can be used as nutritional supplements. They may be used to  
 CC increase stem cell proliferation; to regulate haematopoiesis; and in  
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;  
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and  
 CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid  
 CC sequences of novel human secreted proteins of the invention.  
 XX SQ Sequence 423 AA;  
 Query Match 39.8%; Score 793.5; DB 22; Length 423;  
 Best Local Similarity 45.8%; Pred. No. 2.6e-65;  
 Matches 181; Conservative 60; Mismatches 103; Indels 51; Gaps 14;  
 QY 6 LLLFLALCSAKPF----FSPSHIALKNMMLKDMEDTDDDDDDDDDDDDSLFPTREP 61  
 Db 21 LVSLALSQLPFFQGFQDFDFTLDDGPFMMNDEEASGADTSGVLDPP-----SVTPYS- 74  
 QY 62 RSHFPDFLPMCPGQCYSRVVHCS-DLGLTSVPTNIPDTRMLDQNNKIKEKEND 120  
 Db 75 -----AMCPGCHCHLRVVOCAPTGLKSVPEISPDFTLLDQNNDSLEKDD 124  
 QY 121 FKGLTSLYLNNKTKTHPKAFLTKKLRRLYLHSHNQLSEIPLNPKSLAELRIHEN 180  
 Db 125 FKGLHLYALVNNKISKIHEKAFSPLRKQKLYISQNHVLETPPNLPSLVELRTHDN 184  
 QY 181 KVKTKOKTFKGMALHVLANSANPLDNGIEPGAFECV-----TVFHRTAEAKLTS-VP 235  
 Db 185 RIRKVPKGVFSLRNMNCCIEGMGPLENSGEPGAFDCLNLYTXRLQ--RSKLTHGSP 242  
 QY 236 KGLPPTLELHDYNNKISTVEL-EDFKRYKELQRLGLGNKKITDIENGSLANIPVRREIH 294  
 Db 243 KYLPTNELHLDHNKIOGHTGRDLLRYSKLYRLGLGHNOIRMIENGSLFPLTREHV 302  
 QY 295 LENNKKKIPSGLPKLYQIIF-LHNSNIAVGV-NDFC-----PTVPMKKSL 342  
 Db 303 LDNNKLARVPSPGDKLLQVYVILHNSNIIHOSGVNEFLFPWFGGEAGP-----Y 354  
 QY 343 YSAISLFN-NPVKYWE-MQATFRCVLSRMSVOLG 375  
 Db 355 YNGHSFAFTPLPYWERLQATFRVVTDRLAIQFG 389  
 RESULT 28  
 AAR42266  
 ID AAR42266 standard; Protein: 280 AA.

XX AC AAR42266;  
 XX DT 28-APR-1994 (first entry)  
 XX DE Decorin sequence PT-77 (N-terminal to LRR10).  
 XX KW leucine-rich repeat; proteoglycan; cell regulatory factor; MBP;  
 KW KW decorin; maltose binding protein; tumour growth; inhibition;  
 KW KW decorin; PG-II; PG-40; transforming growth factor-beta; TGF-beta.  
 XX PN WO9320202-A.  
 XX PD 14-OCT-1993.  
 XX PF 02-APR-1993; 93WO-US03171.  
 XX PR 03-APR-1992; 92US-0865652.  
 XX PA (LJOL-) LA JOLLA CANCER RES FOUND.  
 XX PI Cardenas J, Craig W, Mullen DG, Pierschbacher MD;  
 PI Ruoslahti EI;  
 XX DR WPI; 1993-336910/42.  
 XX DR N-PSDB; AAQ50052.  
 XX PT Active fragments of protein esp. decorin - with cell regulatory  
 PT factor domain, useful for inhibiting cell regulatory factor  
 PT activity  
 XX PS Claim 10; Page 47-48; 77pp; English.  
 XX CC Active fragments of decorin (full-length coding sequence AAQ50046)  
 CC were generated by PCR and fused to Maltose Binding Protein. The  
 CC resulting fusion proteins were useful for inhibiting the activity of  
 CC a cell regulatory factor, esp. TGF-beta, and hence for treating  
 CC conditions associated with over-activity of the growth factor such  
 CC as certain tumours.  
 XX SQ Sequence 280 AA;  
 Query Match 39.0%; Score 776; DB 14; Length 280;  
 Best Local Similarity 53.4%; Pred. No. 6.2e-64;  
 Matches 149; Conservative 52; Mismatches 76; Indels 2; Gaps 2;  
 QY 50 DEDNSLFTPREPSHFPFDLPMPGQCYSRVVHCSDLGLTSVPTNIPDTRMLDQ 109  
 Db 3 DEASGGIP-EVDDRDFFESLGPVCFRCQCHLRVVOCSDLGLDKVDPDPTLLDQ 61  
 QY 110 NKKIKETKENDFKGLTSLYLNNKTKTHPKAFLTKKLRRLYLHSHNQLSEIPLNLP 169  
 Db 62 NKKITEKDGFKNLKHALILVNNKISKVSPGAFPLVKKLRLYLSKNQLKELPKMP 121  
 QY 170 KSLAELRIHENKVKTKOKTFKGMALHVLANSANPLDNGIEPGAFECV-TVFHRTAE 228  
 Db 122 KTLQELRAHENEITKVRKVTFNGLNQMIVIELGTNP LKSSGIENGAFQGMKKLSYRIAD 181  
 QY 229 AKLTSVPKGLPPTLELHDYNNKISTVELEDFKRYKELQRLGLGNKKITDIENGSLANTP 288  
 Db 182 TMTISPOGSLTLELHDDGNKISRVDASLKLNNLAKLGLSFSISAVDNGSLANTP 241  
 QY 289 RVREIHLNENKLLKIPSGLPKLYQIIFLHNSNIAVGV 327  
 Db 242 HLRELHLDNNKLTFRVPGGLAEHKYIQVYVYLNHNINISVVG 280  
 RESULT 29  
 AAU20404  
 ID AAU20404 standard; Protein: 128 AA.  
 XX AC AAU20404;  
 XX XX

06-DEC-2001 (first entry)  
 Human secreted protein, Seq ID NO 396.  
 Immunomodulatory; human immunodeficiency virus; HIV; anaemia; angina; rheumatoid arthritis; antiarteriosclerotic; cardiant; vascular; cerebroprotective; thrombolytic; antimicrobial; ophthalmological; cytostatic; Alzheimer's disease; Parkinson's disease; human; multiple sclerosis; cancer; hyperproliferative disorder; infection; Gaucher's disease; neurological disease; cerebrovascular disorder; thrombosis; wound healing.  
 Homo sapiens.  
 WO200155326-A2.  
 02-AUG-2001.  
 17-JAN-2001; 2001WO-US01347.  
 31-JAN-2000; 2000US-0179065.  
 (HUMA-) HUMAN GENOME SCI INC.  
 Rosen CA, Barash SC, Ruben SM;  
 WPI; 2001-451931/48.  
 N-PSDB; AAS33113.  
 New nucleic acids and polypeptides, useful for diagnosing, preventing or treating medical conditions -  
 Claim 11; SEQ ID NO 396; 753pp; English.  
 The invention relates to novel isolated nucleic acid molecules (I) encoding human secreted proteins (II). (I) and (II) are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate expression of secreted proteins. (I) and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples, and so which patients may be in need of restorative therapy. (II) may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of the secreted proteins. The anti-(II) antibodies and antagonists may also be used to down regulate expression and activity of (II). The anti-(II) antibodies may also be used as diagnostic agents for detecting the presence of (II) in samples (e.g. by enzyme linked immunosorbent assay (ELISA)). The disorders include for example: immune/autoimmune diseases (e.g. HIV (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and Parkinson's disease), neurological diseases (e.g. Alzheimer's disease, Gaucher's disease and Charcot-Marie-Tooth disease), cardio-/cerebrovascular disorders (e.g. cardiac arrest, tachycardia, angina and thrombosis), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections). (I) and (II), agonists, antagonists and antibodies can also be used to promote wound healing, maintain organs before transplantation, and support cell culture of primary tissues. AAU20342-AAU20666 represent human secreted protein amino acid sequences, and related sequences of the invention.  
 Note: The sequence data for this patent did not appear in the printed specification but was obtained in electronic format directly from WIPO at: ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 128 AA;

Query Match 32.3%; Score 643; DB 22; Length 128;  
 Best Local Similarity 98.4%; Pred. No. 5.2e-55;  
 Matches 125; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 253 STVELEDFKRYKELQRLGLGNKNTDIENGLANIPIVREIHLENNKIKIPSGLPKLY 312  
 Db 2 STVELEDKRXKELQRLGLGNKNTDIENGLANIPIVREIHLENNKIKIPSGLPKLY 61  
 QY 313 LQIIFLHNSNISTARVGVNDFCTVTPKMKKSLYSALSLENNPVKYWEMOPATFRCVLSRMSV 372  
 Db 62 LQIIFLHNSNISTARVGVNDFCTVTPKMKKSLYSALSLENNPVKYWEMOPATFRCVLSRMSV 121  
 QY 373 QLGNFGM 379  
 Db 122 QLGNFGM 128  
 RESULT 30  
 AAR42265  
 ID AAR42265 standard; Protein; 234 AA.  
 XX  
 AC AAR42265;  
 XX  
 DT 28-APR-1994 (first entry)  
 XX  
 DE Decorin sequence PT-76 (N-terminal to LRR8).  
 XX  
 KW leucine-rich repeat; proteoglycan; cell regulatory factor; MBP;  
 KW fusion protein; maltose binding protein; tumour growth; inhibition;  
 KW decorin; PG-II; PG-40; transforming growth factor-beta; TGF-beta.  
 XX  
 PN WO9320202-A.  
 XX  
 PD 14-OCT-1993.  
 XX  
 PF 02-APR-1993; 93WO-US03171.  
 XX  
 PR 03-APR-1992; 92US-0865652.  
 XX  
 PA (LJOL-) LA JOLLA CANCER RES FOUND.  
 XX  
 PI Cardenas J, Craig W, Mullen DG, Pierschbacher MD;  
 PI Ruoslahti EI;  
 XX  
 DR WPI; 1993-336910/42.  
 DR N-PSDB; AAQ50051.  
 XX  
 PT Active fragments of protein esp. decorin - with cell regulatory  
 PT factor domain, useful for inhibiting cell regulatory factor  
 PT activity  
 XX  
 PS Claim 10; Page 45-46; 77pp; English.  
 XX  
 PS Active fragments of decorin (full-length coding sequence AAQ50046)  
 CC were generated by PCR and fused to Maltose Binding Protein. The  
 CC resulting fusion proteins were useful for inhibiting the activity of  
 CC a cell regulatory factor, esp. TGF-beta, and hence for treating  
 CC conditions associated with over-activity of the growth factor such  
 CC as certain tumours.  
 XX  
 SQ Sequence 234 AA;  
 Query Match 30.9%; Score 616; DB 14; Length 234;  
 Best Local Similarity 52.4%; Pred. No. 4e-49;  
 Matches 122; Conservative 40; Mismatches 69; Indels 2; Gaps 2;  
 QY 50 DEONSLFFTEPRESHFFPDLFPMCFPGCCYRVVHCSDGLGTSVPTNIPDTRMLDLQ 109  
 Db 3 DEASGICP-EVPDRDFPSPGLGVCPCRCOHLRVQCSDGLGDKVPKDLPPDPTLLDLQ 61  
 QY 110 NNRKIKENDFKGLTSLYGLILNNKLTIKHPKAFLTTKLRRLYLHSHNOLSEIFLNLP 169  
 Db 62 NNRKITEKDGDFKNLNLHALLILNNKISKVSPCATPLVKLERLYLSNQLKELPEKMP 121  
 QY 170 KSLAEIRIHENKYYKIOKDTFGKGNALHVLMSANPLDNNIEPGAFEGV-TVFHIRIAE 228  
 Db 122 KTLQELRAHENEITKVRKVTFTNGLNQMIYELGTNPLKSSGIENGAFQGMKLSYRIAD 181

QY	229	AKLTVKGLPPTLEHLHLNKNKISTVELEDFKRYKELQRLGKLNKNTIDTEN	281
Db	182	TNITSIPQGLPSELHLNKNKISRDVAASLKLGLNKLKGLSFGNSISAVDN	234
RESULT 31			
AAG00241			
ID	AAG00241	standard; Protein: 88 AA.	
XX	AC	AAG00241;	
XX	AC	AAG00241;	
XX	DT	06-OCT-2000 (first entry)	
XX	DE	Human secreted protein, SEQ ID NO: 4322.	
DE	XX		
XX	XX	Human; 5' EST; expressed sequence tag; secreted protein; cdna isolation;	
KW	KW	gene therapy; chromosome mapping.	
KW	KW	gene therapy; chromosome mapping.	
XX	XX	Homo sapiens.	
XX	OS		
XX	XX	EP1033401-A2.	
PN	PN		
XX	XX	06-SEP-2000.	
XX	PD		
XX	XX	21-FEB-2000; 2000EP-0200610.	
XX	XX	26-FEB-1999; 99US-0122487.	
PR	PR	(GEST ) GENSET.	
XX	XX	Dumas Milne Edwards J, Duclert A, Giordano J;	
PI	PI	WPI; 2000-500381/45.	
XX	XX	N-PSDB; AAC00247.	
XX	XX		
XX	XX	New nucleic acid that is a 5' expressed sequence tag (5' EST) for	
PT	PT	obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for	
PT	PT	diagnostic, forensic, gene therapy and chromosome mapping procedures -	
XX	XX	Claim 13; SEQ ID 4322; 71pp + CD-ROM; English.	
XX	XX		
XX	XX	The present sequence is a polypeptide encoded by one of a large number	
CC	CC	of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs	
CC	CC	were prepared from total human RNAs or polyA+ RNAs derived from 30	
CC	CC	different tissues. EST sequences usually correspond mainly to the 3'	
CC	CC	untranslated region (UTR) of the mRNA because they are often obtained	
CC	CC	from oligo-dT primed cDNA libraries. Such ESTs are not well suited for	
CC	CC	isolating cDNA sequences derived from the 5' ends of mRNAs and even in	
CC	CC	those cases where longer cDNA sequences have been obtained, the full 5'	
CC	CC	UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'	
CC	CC	ends and can therefore be used to obtain full length cDNAs and genomic	
CC	CC	DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and	
CC	CC	chromosome mapping procedures. They are used to obtain upstream	
CC	CC	regulatory sequences and to design expression and secretion vectors.	
XX	XX	Sequence 88 AA;	
SQ	SQ		
Query Match 24.7%; Score 493; DB 21; Length 88;			
Best Local Similarity 100.0%; Pred. No. 3e-38;			
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	MKEYVLLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDNSLFTPRE	60
Db	1	MKEYVLLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDNSLFTPRE	60
QY	61	PRSHFFPFDLFPWCPFGCQCYSRVVHCS	88
Db	61	PRSHFFPFDLFPWCPFGCQCYSRVVHCS	88
RESULT 32			
AAY64720			
ID	AAY64720	standard; Protein: 88 AA.	
XX	AC	AAY64720;	
XX	DT	01-FEB-2000 (first entry)	
XX	DE	Human 5' EST related polypeptide SEQ ID NO:881.	
DE	XX		
XX	XX	Human; 5' EST; expressed sequence tag; secreted protein; diagnosis;	
KW	KW	gene therapy; chromosome mapping; upstream regulatory sequence;	
KW	KW	forensic; location; development; protein synthesis; stability;	
KW	KW	regulation; identification.	
XX	XX	Homo sapiens.	
OS	OS		
XX	XX	WO9953051-A2.	
PN	PN		
XX	XX	21-OCT-1999.	
XX	XX	09-APR-1999; 99WO-1B00712.	
XX	XX	09-APR-1998; 98US-0057719.	
PR	PR	28-APR-1998; 98US-0069047.	
XX	XX	(GEST ) GENSET.	
XX	XX	Dumas Milne Edwards J, Duclert A, Giordano J;	
PI	PI	WPI; 2000-038446/03.	
XX	XX	N-PSDB; AAZ42334.	
DR	DR		
XX	XX	Novel secreted protein 5' expressed sequence tag sequences used in	
PT	PT	diagnostic, forensic, gene therapy, and chromosome mapping procedures	
XX	XX	Claim 3; Page 621; 837pp; English.	
XX	XX		
XX	XX	AAZ42265 to AAZ43075 represent novel 5' expressed sequence tag (EST)	
CC	CC	sequences, corresponding to human secreted proteins. AAY64651 to	
CC	CC	AAY65438 represent the EST-related proteins corresponding to AAZ42265 to	
CC	CC	AAZ43052. The 5' ESTs can be used for producing secreted human gene	
CC	CC	products. They can be used to identify and isolate 5' untranslated	
CC	CC	regions (UTRs) and upstream regulatory regions which control the	
CC	CC	location, development stage, rate, and quantity of protein synthesis, as	
CC	CC	well as stability of mRNA. The ESTs are also useful as probes for	
CC	CC	chromosome mapping, and to obtain full length cDNA clones. The ESTs can	
CC	CC	also be used in forensic procedures to identify individuals, or in	
CC	CC	diagnostic procedures to identify individuals having genetic diseases	
CC	CC	resulting from abnormal gene expression. The products may also be used in	
CC	CC	gene therapy protocols. The nucleic acids encoding signal peptides can be	
CC	CC	used for directing extracellular secretion of a polypeptide or the	
CC	CC	insertion of a polypeptide into a membrane, or importing a polypeptide	
CC	CC	into a cell. The proteins encoded by the EST sequences may be useful in	
CC	CC	treating a variety of human conditions. Secreted proteins have	
CC	CC	therapeutic value, and the identification of new secreted proteins is	
CC	CC	valuable. AAZ42249 to AAZ42264 and AAY64644 to AAY64650 represent	
CC	CC	sequences used in the exemplification of the present invention.	
XX	XX	Sequence 88 AA;	
SQ	SQ		
Query Match 24.7%; Score 493; DB 21; Length 88;			
Best Local Similarity 100.0%; Pred. No. 3e-38;</			



KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;  
KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;  
KW immune disorder; hematopoietic cell disorder; autoimmune disorder;  
KW allergic reaction; graft versus host disease; organ rejection;  
KW hemostatic; thrombolytic; cardiovascular disorder; infection;  
KW neurological disease; drug screening.  
XX Homo sapiens.  
XX WO20005350-A1.  
XX 21-SEP-2000.  
XX 08-MAR-2000; 2000WO-US05882.  
XX 12-MAR-1999; 99US-0124270.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Rosen CA, Ruben SM;  
XX WPI; 2000-587533/55.  
XX N-PSDB; AAC78325.  
XX Novel isolated nucleic acids comprising sequences encoding peptides  
XX useful for treating or diagnosing e.g. cancer -  
XX Claim 11; Page 2238-2239; 2352pp; English.  
XX AAC77607 to AAC78448 encode the human cancer associated proteins given  
XX in AAB43398 to AAB44239. The proteins can have activities based on the  
XX tissues and cells the genes are expressed in. Example of activities  
XX include: cytostatic; proliferative; vulnerary; immunomodulator;  
XX antidiabetic; antiasthmatic; antirheumatic; antiarthritic;  
XX antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;  
XX dermatological; neuroprotective; cardiant; thrombolytic; coagulant;  
XX nootropic; vasotropic; antipsoriatic and antiangiogenic. The  
XX polynucleotides and polypeptides can be used for preventing, treating or  
XX ameliorating medical conditions and diagnosing pathological conditions.  
XX Polynucleotides, polypeptides, antibodies, agonists and antagonists from  
XX the present invention may be used to treat immune disorders by activating  
XX or inhibiting the proliferation, differentiation or mobilisation of  
XX immune cells, to treat disorders of haematopoietic cells, autoimmune  
XX disorders, allergic reactions, graft versus host disease and organ  
XX rejection, modulate haemostatic or thrombolytic activity, modulate  
XX inflammation, cancers, cardiovascular disorders, neurological disease and  
XX bacterial or viral infections. The peptides, nucleotides, antibodies,  
XX agonists and antagonists may be also be used in drug screens. AAC78449 to  
XX AAC78457 and AAB44240 represent sequences used in the exemplification of  
XX the present invention.  
XX SQ Sequence 155 AA;  
XX Best Match 20.4%; Score 406.5; DB 21; Length 155;  
XX Best Local Similarity 50.3%; Pred. No. 7.6e-30;  
XX Matches 77; Conservative 33; Mismatches 42; Indels 1; Gaps 1;  
QY 176 RIHENVKVKIKQDKFGKGNALHVLVEMSANPLDNNNGIEPGAFEGY-TVFHRIAEAKLTVS 234  
Db 1 RAHENEITKVRKVTFNGLNQMVIELGTNPLKSSGIENGAFQGMKLSYRIADTNITSI 60  
QY 235 PKGLPPTLLEHLDYNKISTVELEDFKRYKELQRLGKNNKIITDIENGSLANIPRVREIH 294  
Db 61 PQGLPPSLTEHLDGKNTISRVDAAASLGNLNLAKLGLSFNSISAVDNGSLANTPHLRELH 120  
QY 295 LENNLKIKPSGLPELKYLIQIFLHNSNIARVG 327  
Db 121 LDNNKLTRVPGLOSIIKXXGGYLNHNHISVVG 153  
RESULT 36  
AAV67598  
ID AAV67598 standard; Protein; 699 AA.

XX AAV67598;  
XX 13-JUN-2000 (first entry)  
XX Human adipose tissue protein #1.  
XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;  
XX arteriosclerosis; hyperuricemia; sleep apnea syndrome.  
XX Homo sapiens.  
XX JP2000037190-A.  
XX 08-FEB-2000.  
XX 23-JUL-1998; 98JP-0225228.  
XX 23-JUL-1998; 98JP-0225228.  
XX (NISB ) JAPAN TOBACCO INC.  
XX WPI; 2000-306578/27.  
XX N-PSDB; AAZ90631.  
XX A physiologically active protein specifically derived from mammal  
XX tissue -  
XX Claim 4; Page 24-27; 50pp; Japanese.  
XX The invention relates to identification of genes and proteins of adipose  
XX tissue relating to obesity, particularly complications of visceral  
XX obesity including diabetes, hyperlipemia, hypertension,  
XX arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes  
XX (AAZ90631-633) and the proteins (AAV67598-67600) are used in the genetic  
XX diagnosis, prevention and treatment of adipose tissue related diseases.  
XX SQ Sequence 699 AA;  
XX Best Match 20.0%; Score 397.5; DB 21; Length 699;  
XX Best Local Similarity 24.9%; Pred. No. 4.3e-28;  
XX Matches 108; Conservative 77; Mismatches 148; Indels 101; Gaps 8;  
QY 32 KMEDTDDDDDDDDDDDDNSL-----FTREPRSHFFFDLFP-----MCPFGC 78  
Db 270 FEEDEEEEGEEDDEEDPVRGDMFRMPSP-----LPAPRGTLRLPGC 320  
QY 79 QCYSRVHCSDLGTSVPTNPFPDTRMLDLQNNKIKETKENDFKGLTSLYLNNKLT 138  
Db 321 SLSYRTISINAMLTQIPPLTAPQITSLTGNSTASIPDEAFNGLPNERLDLSKNIT 380  
QY 139 K--IHPKAFLTTKLRLRYLSHNLSEIPLNPKSLAEIRHENKVKIKQDKTFKGMAL 196  
Db 381 SSGIGPKAFKLLKMLRNMDCNNLIQPSQLPSTLEELKVNENNLOADESLDNLQ 440  
QY 197 HVLEWSANPLDNNNGTEPGAFEGY-TVFHRIAEAKLTVKPGCLPTLLEHLDYNKISTV 255  
Db 441 VTELEGNLSEANYNPLAFKPLKSLAYLRGKKNFRITPOGLPGSIEBELYLENNQIEI 500  
QY 256 ELEDKRYKELQRLGKNNKI-----TDIENGSLANIP----- 288  
Db 501 TELCFNHTKINIVIVLRNKNIEENRIAPLAWINQENLESIDLKYNKLYHVPYSLKSLH 560  
QY 289 -----RVREIHLNNKL 300  
Db 561 LVLLGNGQIERIPGYVFGHMEPGLEYIYLSFNKLADGMDRVSVFYGAYHSIRLEFLDNDL 620  
QY 301 KKIPSGLPKLYLIQIFLHNSNIARVGNDFCTVPKMKKSLYSALSIFNNPVKWMOP 360  
Db 621 KSPGQIQEMKALHURLNANNIRNIPLEIC-NAEEDDDSMLEHLHLENNYIKITREIPS 679  
QY 361 ATRFCVLSRMSVOL 374  
|| | | | |

Db	680	YTFSCIRSYSSIVL 693	
RESULT 37			
AAAB43535			
Id	AAAB43535	standard; Protein; 353 AA.	
XX	AAAB43535;		
AC	AAAB43535;		
DT	08-FEB-2001	(first entry)	
XX	Human cancer associated protein sequence SEQ ID NO:980.		
DE	Human; cancer associated gene; cancer antigen; detection; cancer;		
KW	diagnosis; cytostatic; proliferative; vulnary; immunomodulator;		
KW	antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;		
KW	antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;		
KW	dermatological; neuoroprotective; thrombolytic; coagulant; nootropic;		
KW	vasotopic; antipsoriatic; antiangiogenic; gene therapy; inflammation;		
KW	immune disorder; haematopoietic cell disorder; autoimmune disorder;		
KW	allergic reaction; graft versus host disease; organ rejection;		
KW	haemostatic; thrombolytic; cardiovascular disorder; infection;		
KW	neurological disease; drug screening.		
XX	Homo sapiens.		
OS			
XX	WO200055350-A1.		
PN			
XX	21-SEP-2000.		
PD			
XX	08-MAR-2000; 2000WO-US05882.		
PF			
XX	12-MAR-1999; 99US-0124270.		
PR			
XX	(HUMA-) HUMAN GENOME SCI INC.		
PA			
XX	Rosen CA, Ruben SM;		
PI			
XX	WPI; 2000-587533/55.		
DR	N-PSDB; AAC77744.		
XX			
XX	Novel isolated nucleic acids comprising sequences encoding peptides		
PT	useful for treating or diagnosing e.g. cancer -		
XX			
PS	Claim 11; Page 1552-1553; 2352pp; English.		
XX			
CC	AAAC77607 to AAC78448 encode the human cancer associated proteins given		
CC	in AAB43398 to AAB44239. The proteins can have activities based on the		
CC	tissues and cells the genes are expressed in. Example of activities		
CC	include: cytostatic; proliferative; vulnary; immunomodulator;		
CC	antidiabetic; antiasthmatic; antirheumatic; antiarthritic;		
CC	antiinflammatory; antithyroid; antiallergic; antibacterial;		
CC	dermatological; neuoroprotective; cardiant; thrombolytic; coagulant;		
CC	nootropic; vasotopic; antipsoriatic and antiangiogenic. The		
CC	polynucleotides and polypeptides can be used for preventing, treating or		
CC	ameliorating medical conditions and diagnosing pathological conditions.		
CC	Polynucleotides, polypeptides, antibodies, agonists and antagonists from		
CC	the present invention may be used to treat immune disorders by activating		
CC	or inhibiting the proliferation, differentiation or mobilisation of		
CC	immune cells, to treat disorders of haematopoietic cells, autoimmune		
CC	disorders, allergic reactions, graft versus host disease and organ		
CC	rejection, modulate haemostatic or thrombolytic activity, modulate		
CC	inflammation, cancers, cardiovascular disorders, neurological disease and		
CC	bacterial or viral infections. The peptides, nucleotides, antibodies,		
CC	agonists and antagonists may be also be used in drug screens. AAC78449 to		
CC	AAC78457 and AAB44240 represent sequences used in the exemplification of		
CC	the present invention.		
XX			
SQ	Sequence 353 AA;		
Query Match	19.7%; Score 393; DB 21; Length 353;		
Best Local Similarity	31.7%; Pred No. 4,3e-28;		
Matches 102; Conservative	70; Mismatches 128; Indels 22; Gaps 10;		

CC subjects bearing a vascularised tumour, polycystic kidney disease,  
 CC diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse  
 CC and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and  
 CC ABB90721-ABB90789) are disclosed, as are marker oligonucleotide  
 CC sequences; tumour endothelial markers (TEM) ABL91996-ABL92041 and  
 CC ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074;  
 CC and pan-endothelial markers (PEM) ABL91903-ABL91995.  
 XX  
 SQ Sequence 338 AA;  
 Query Match 19.6%; Score 390; DB 23; Length 338;  
 Best Local Similarity 31.8%; Pred. No. 7.8e-28;  
 Matches 100; Conservative 70; Mismatches 122; Indels 22; Gaps 10;  
 Qy 66 FPDLEF---PWCDFGQC---YSRVHCSDLGLTSVPTNIPDFTMLDLQNNKIKEIKE 118  
 Db 25 FPLSYGSSPCAPCEPCPEPSYAMCYDELKLSVPM-VPPGKLYLYLRNQIDHIDE 83  
 Qy 119 NDFKGLTSLYGLILNNKLT--TKIHPKAFITTKLRRLYLHSHNQLSEIPLNPKSLAELR 176  
 Db 84 KAFENVDTQLWLIDHNLNLSKIKGRVFSKQLKQLKHLHNNHNLTSVGLPKSLEDIQ 143  
 Qy 177 IHENKVKKIQTDFKGMNALHVLMSANPLDNGNIEGAFEGV-TVFHRIAEAKLTSVP 235  
 Db 144 LTHNKITKL--GSFEGVLNLTFIHQLHNLKEDAVS-AAFKGLKSLYLELDLSEFNQIARLP 200  
 Qy 236 KGLPPTLELHLDYNNKISTVELEDFKRYKELQRLGLGNKKTIDTE-NGSLANIPRVREIH 294  
 Db 201 SGLPVSLLTLYLDNNKISNIPDEYFKRFNALQYLRSHNELADSGIPGNSFVSSLVELD 260  
 Qy 295 LENNKKKIPSGLPKELK--YLIQIIFLHNSIARVGNDFCPTVPKMKKSLYSALSIFNFP 352  
 Db 261 LSYNKLKNIPTVNNLENLYLEV-----NOLEKFDIKSFCKILGILPLSVSKIKHLRLDGNR 315  
 Qy 353 VKYWMQPATRCV 366  
 Db 316 ISETSLPPDMYECL 329  
 RESULT 39  
 AAG73881  
 ID AAG73881 standard; Protein; 353 AA.  
 AC AAG73881;  
 XX  
 DT 03-SEP-2001 (first entry)  
 XX  
 DE Human colon cancer antigen protein SEQ ID NO:4645.  
 XX  
 KW Human; colon cancer; colon cancer antigen; diagnosis: detection;  
 KW colorectal carcinoma; chromosome 12.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200122920-A2.  
 XX  
 PD 05-APR-2001.  
 XX  
 PF 28-SEP-2000; 2000WO-US26524.  
 XX  
 PR 29-SEP-1999; 99US-0157137.  
 PR 03-NOV-1999; 99US-0163280.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Ruben SM, Barash SC, Birse CE, Rosen CA;  
 XX WPI; 2001-235357/24.  
 DR N-PSDB; AAB33312.  
 XX  
 XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,  
 XX useful for preventing, diagnosing and/or treating colorectal cancers -

PS  
 XX Claim 11; Page 6448-6450; 9803pp; English.  
 CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon  
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where  
 CC the proteins are collectively known as colon cancer antigens. The colon  
 CC cancer antigens have cytostatic activity and can be used in gene  
 CC therapy and vaccine production. N and P may be used in the prevention,  
 CC diagnosis and treatment of diseases associated with inappropriate P  
 CC expression. For example, N and P may be used to treat disorders  
 CC associated with decreased expression by rectifying mutations or deletions  
 CC in a patient's genome that affect the activity of P by expressing  
 CC inactive proteins or to supplement the patients own production of P.  
 CC Additionally, N may be used to produce the colon cancer-associated Ps,  
 CC by inserting the nucleic acids into a host cell and culturing the cell  
 CC to express the proteins. N and P can be used in the prevention, diagnosis  
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204  
 CC and AAB7789 represent sequences used in the exemplification of the  
 CC present invention.  
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were  
 CC missing at time of publication, meaning no sequences are present for  
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.  
 XX  
 SQ Sequence 353 AA;  
 Query Match 19.6%; Score 390; DB 22; Length 353;  
 Best Local Similarity 31.8%; Pred. No. 8.3e-28;  
 Matches 100; Conservative 70; Mismatches 122; Indels 22; Gaps 10;  
 Qy 66 FPDLEF---PWCDFGQC---YSRVHCSDLGLTSVPTNIPDFTMLDLQNNKIKEIKE 118  
 Db 40 FPLSYGSSPCAPCEPCPEPSYAMCYDELKLSVPM-VPPGKLYLYLRNQIDHIDE 98  
 Qy 119 NDFKGLTSLYGLILNNKLT--TKIHPKAFITTKLRRLYLHSHNQLSEIPLNPKSLAELR 176  
 Db 99 KAFENVDTQLWLIDHNLNLSKIKGRVFSKQLKQLKHLHNNHNLTSVGLPKSLEDIQ 158  
 Qy 177 IHENKVKKIQTDFKGMNALHVLMSANPLDNGNIEGAFEGV-TVFHRIAEAKLTSVP 235  
 Db 159 LTHNKITKL--GSFEGVLNLTFIHQLHNLKEDAVS-AAFKGLKSLYLELDLSEFNQIARLP 215  
 Qy 236 KGLPPTLELHLDYNNKISTVELEDFKRYKELQRLGLGNKKTIDTE-NGSLANIPRVREIH 294  
 Db 216 SGLPVSLLTLYLDNNKISNIPDEYFKRFNALQYLRSHNELADSGIPGNSFVSSLVELD 275  
 Qy 295 LENNKKKIPSGLPKELK--YLIQIIFLHNSIARVGNDFCPTVPKMKKSLYSALSIFNFP 352  
 Db 276 LSYNKLKNIPTVNNLENLYLEV-----NOLEKFDIKSFCKILGILPLSVSKIKHLRLDGNR 330  
 Qy 353 VKYWMQPATRCV 366  
 Db 331 ISETSLPPDMYECL 344  
 RESULT 40  
 AAR42263  
 ID AAR42263 standard; Protein; 139 AA.  
 XX  
 AC AAR42263;  
 XX  
 DT 28-APR-1994 (first entry)  
 XX  
 DE Decorin sequence PT-74 (N-terminal to LRR4).  
 XX  
 KW leucine-rich repeat; proteoglycan; cell regulatory factor; MBP;  
 KW fusion protein; maltose binding protein; tumour growth; inhibition;  
 KW decorin; PG-II; PG-40; transforming growth factor-beta; TGF-beta.  
 XX  
 PN WO9320202-A.  
 XX  
 PD 14-OCT-1993.  
 XX  
 PF 02-APR-1993; 93WO-US03171.  
 XX



PR 03-APR-1992; 92US-0865652.  
 XX (LJOL-) LA JOLLA CANCER RES FOUND.  
 PA Cardenas J, Craig W, Mullen DG, Pierschbacher MD;  
 PI Ruoslahti EI;  
 XX WPI; 1993-336910/42.  
 DR N-PSDB; AAO50049.  
 XX  
 PT Active fragments of protein esp. decorin - with cell regulatory  
 PT factor domain, useful for inhibiting cell regulatory factor  
 XX activity  
 XX  
 PS Claim 10; Page 41; 77pp; English.  
 XX  
 CC Active fragments of decorin (full-length coding sequence AAO50046)  
 CC were generated by PCR and fused to Maltose Binding Protein. The  
 CC resulting fusion proteins were useful for inhibiting the activity of  
 CC a cell regulatory factor, esp. TGF-beta, and hence for treating  
 CC conditions associated with over-activity of the growth factor such  
 CC as certain tumours.  
 XX  
 SQ Sequence 139 AA;

Query Match 19.3%; Score 384.5; DB 14; Length 139;  
 Best Local Similarity 55.1%; Pred. No. 7.3e-28;  
 Matches 76; Conservative 20; Mismatches 41; Indels 1; Gaps 1;  
 QY 50 DDNSLFTTREPSSHFFPDLFPMCPGOCYKRVHCHSDGLTSVPTNIPFDTRMLDLQ 109  
 Db 3 DEASIGP-EVPDDRDFEPLSGVPCPFCQCCHLRVQCSDLGLDKVPKDLPPDTTLLDLQ 61  
 QY 110 NKKIKKIKENDFKGLTSLYGLILNNKLTHTPKAFLTTKRLRLYLHSHNLSLPIPLNP 169  
 Db 62 NKKITEIKDGFKNLKNLHLLVNNKLSKVSFGAFTPLVKLERLYLSKNQKELPEKMP 121  
 QY 170 KSLAELRIHENVKVKIQK 187  
 Db 122 KTLQELRAHENEITKVRK 139

RESULT 41  
 AAY05767  
 ID AAY05767 standard; Protein; 421 AA.  
 XX  
 AC AAY05767;  
 XX  
 DT 19-JUL-1999 (first entry)  
 XX  
 DE Human osteomodulin PRO216.  
 XX  
 KW Osteomodulin; fibromodulin; PRO216; human; angiogenesis;  
 KW cardiovascularisation; wound healing; cancer; atherosclerosis;  
 KW cardiac hypertrophy; myocardial infarction; antiangiogenic;  
 KW antitumour; tissue regeneration; pulmonary fibrosis;  
 KW neurological disease; macular degeneration; diagnosis; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO9914234-A2.  
 XX  
 PD 25-MAR-1999.  
 XX  
 XX 14-SEP-1998; 98WO-US19177.  
 XX  
 XX 24-NOV-1997; 97US-0066772.  
 PR 17-SEP-1997; 97US-0059117.  
 PR 27-OCT-1997; 97US-0063329.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Fong S, Gerritsen ME, Goddard A, Gurney AL, Hillan K;

PI Williams PM, Woodwi;  
 XX  
 DR WPI; 1999-254381/21.  
 DR N-PSDB; AAX25439.  
 XX  
 PT Composition containing human polypeptides with anti-angiogenic  
 PT activity  
 XX  
 PS Example 1; Fig 6; 102pp; English.  
 XX  
 CC The present sequence represents human PRO216, which was identified  
 CC as human osteomodulin. The sequence is predicted from cDNA clone  
 CC UNQ190 or DNA33087-1158 (ATCC 209381, see AAX25439). Compositions  
 CC containing PRO216, PRO230 (see AAY05764) and PRO302 (see AAY05768) in  
 CC admixture with a carrier are claimed. The compositions are used to  
 CC treat or prevent a wide range of cardiovascular, endothelial and  
 CC angiogenic disorders (claimed), specifically cardiac hypertrophy  
 CC (especially where associated with elevated levels of prostaglandin  
 CC F2 alpha or induced by myocardial infarction), trauma (wounds,  
 CC burns, or tissue regeneration more generally, including neurological  
 CC disease), and cancer. Antagonists may be used similarly, also to  
 CC treat age-related macular degeneration (or other angiogenic retinal  
 CC disorders) and to prevent excessive growth of connective tissue  
 CC during wound healing or in pulmonary fibrosis.  
 XX  
 SQ Sequence 421 AA;

Query Match 18.4%; Score 366; DB 20; Length 421;  
 Best Local Similarity 29.3%; Pred. No. 1.8e-25;  
 Matches 95; Conservative 73; Mismatches 138; Indels 18; Gaps 8;  
 QY 41 DDDDDDDDDDDNSLFTTREPSSHFFPDLFPM-CFPGCQC---YSRVVHCHSDGLTSVP 96  
 Db 28 DEDYDQDDDDYQTFPFRQNVYGVPPFQHYTLGCVSECFCTPFPSSMYCDNRKLTIP 87  
 QY 97 TNPFTDRLMDLNNKIKENDFKGLTSLYGLILNNKLTHTPKAFLTTKRLRL 154  
 Db 88 -NTPMHIQQLYLOFNEIEAVTNSFTNATHLKEINSHNKIRSKQIDYGVAKLPNLLQ 146  
 QY 155 YLSHNSLSEIPLNPKSLAELRIHENVKVKIKQDKTFKGMNALHLEMSANPLDNGIEPG 214  
 Db 147 HLEHNNLEFPFPLPKSLERLLGYNEISKLOTNMDGLVNLTMLDLCYNLHDSLLDKK 206  
 QY 215 APEGV-TVPHIRIAEAKLTVPKGLPPTLLEHLHLDYKNKISTVELEDFKRYKELORGLGN 273  
 Db 207 IFAKMEKIMQNLCSNRLESMPGLPSSLMYLSLENNSSISPEKYFDKLPKLHTRMSH 266  
 QY 274 NKITDIENGLANIPRVREIHLNENKLLK---IPSGLPKLYLIIFLHNSNIAIRGVND 330  
 Db 267 NKLQDIPY-NIFNLPNIVELSVCHNKLKQAFYIPRNLEHL-----YLNNEIEKMNLTIV 319  
 QY 331 FCPVTPKMKKSLYSALSFPNVPK 354  
 Db 320 MCPSIDPLHYHLLTYIRVDQNKLK 343

RESULT 42  
 AAB33417  
 ID AAB33417 standard; Protein; 421 AA.  
 XX  
 AC AAB33417;  
 XX  
 DT 29-JAN-2001 (first entry)  
 XX  
 DE Human PRO216 protein UNQ190 SEQ ID NO:19.  
 XX  
 KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;  
 KW dermatological; antiarthritic; anti rheumatic; immunosuppressive;  
 KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;  
 KW antianemic; hepatotropic; virucide; antipsoriasis; antiallergic;  
 KW antischmatic; systemic lupus erythematosus; rheumatoid arthritis;  
 KW osteoarthritis; spondyloarthopathy; systemic sclerosis; sarcoidosis;  
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;

KW	systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW	autoimmune thrombocytopaenia; immune-mediated renal disease;
KW	demyelinating disease; hepatobiliary disease; Whipple's disease;
KW	inflammatory bowel disease; gluten-sensitive enteropathy;
KW	autoimmune disease; immune-mediated skin disease; allergic disease;
KW	immunological disease; transplantation associated disease;
KW	graft rejection; graft-versus-host-disease.
XX	
XX	Homo sapiens.
OS	
XX	WO2000053758-A2.
PN	
XX	14-SEP-2000.
PD	
XX	
XX	02-MAR-2000; 200WO-US05841.
XX	
XX	08-MAR-1999; 99WO-US05028.
PR	10-MAR-1999; 99US-0123618.
PR	12-MAR-1999; 99US-0123957.
PR	23-MAR-1999; 99US-0125775.
PR	12-APR-1999; 99US-0128849.
PR	20-APR-1999; 99WO-US08615.
PR	28-APR-1999; 99US-0131445.
PR	04-MAY-1999; 99US-0132371.
PR	14-MAY-1999; 99US-0134287.
PR	02-JUN-1999; 99WO-US12252.
PR	23-JUN-1999; 99US-0141037.
PR	20-JUL-1999; 99US-0144758.
PR	26-JUL-1999; 99US-0145698.
PR	28-JUL-1999; 99US-0146222.
PR	01-SEP-1999; 99WO-US20111.
PR	08-SEP-1999; 99WO-US20594.
PR	13-SEP-1999; 99WO-US20944.
PR	15-SEP-1999; 99WO-US21090.
PR	15-SEP-1999; 99WO-US21547.
PR	05-OCT-1999; 99WO-US23089.
PR	29-OCT-1999; 99US-0162506.
PR	29-NOV-1999; 99WO-US28214.
PR	30-NOV-1999; 99WO-US28313.
PR	30-NOV-1999; 99WO-US28409.
PR	01-DEC-1999; 99WO-US28301.
PR	01-DEC-1999; 99WO-US28634.
PR	02-DEC-1999; 99WO-US28551.
PR	02-DEC-1999; 99WO-US28564.
PR	02-DEC-1999; 99WO-US28565.
PR	16-DEC-1999; 99WO-US30095.
PR	20-DEC-1999; 99WO-US30999.
PR	30-DEC-1999; 99WO-US31274.
PR	05-JAN-2000; 200WO-US00219.
PR	06-JAN-2000; 200WO-US00277.
PR	06-JAN-2000; 200WO-US00376.
PR	11-FEB-2000; 200WO-US03565.
PR	18-FEB-2000; 200WO-US04341.
PR	18-FEB-2000; 200WO-US04342.
PR	22-FEB-2000; 200WO-US04414.
XX	
XX	(GETH ) GENENTECH INC.
PA	
XX	Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
PI	Kabatoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
PI	Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
PI	
XX	WPI; 2000-572271/53.
DR	N-PSDB; AAC58582.
DR	
XX	
XX	Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT	immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
PT	arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
XX	
XX	Claim 33; Fig 8; 309pp; English.
PS	
XX	
CC	The present invention describes sixty four human PRO proteins which can
CC	be used in the treatment of immune related diseases. The human PRO

QY	331	FCPTVPKMKSLYSALSLENNPVK	354
	: :	:   :   :   :	
Db	320	MCFSIDPLHYHHLTIRVDONKLK	343
RESULT	44		
AAAY88377			
ID	AAAY88377 standard; Protein; 421 AA.		
AC	AAAY88377;		
XX	20-JUL-2000 (first entry)		
DE	PRO216 (osteomodulin/fibromodulin homologue) protein sequence.		
XX			
KW	Human; PRO216; Osteomodulin; fibromodulin; homologue; cardiact; angiogenic; cytotatic; ophthalmic; antiproliferative activity; cardiovascular; endothelial; angiogenic disorder; cardiac hypertrophy; trauma; cancer; myocardial infarction; age-related macular degeneration.		
OS	Homo sapiens.		
XX	WO200015792-A2.		
PN	23-MAR-2000..		
PD			
PF	13-SEP-1999; 99WO-US20944..		
XX			
PR	14-SEP-1998; 98US-0100262.		
PR	14-SEP-1998; 98WO-US19177.		
XX			
PA	(GEPH ) GENENTECH INC.		
Fong S,	Gerritsen MB,	Goddard A,	Gurney AL, Hillan KJ;
PI	Williams PW,	Wood WI;	
XX			
WI:	2000-271431/23.		
N-PSDB:	AAA13198.		
XX			
A	composition comprising PRO230, PRO216 or PRO302 polypeptides, agonists or antagonists useful for promotion or inhibition of cardiovascularisation, angiogenesis or endothelialisation in mammals - Example 2; Fig 4; 135pp; English.		
XX			
This	sequence represents the human PRO216 amino acid sequence. PRO216 is a human osteomodulin/fibromodulin homologue. The invention relates to a composition comprising a PRO230 (tubulointerstitial nephritis antigen homologue), PRO216 (osteomodulin/fibromodulin homologue) or PRO302 (vitellogenic carboxypeptidase homologue) polypeptide, or an agonist or antagonist of these. Also included in the invention is a method for preparing the composition, agonists and antagonists of PRO230, PRO216 or PRO302, and antibodies that bind to a PRO230, PRO216 or PRO302 polypeptides. The composition of the invention has cardiant, angiogenic, cytotatic, ophthalmic, and antiproliferative activity. Analysis of the level of expression of a gene encoding a PRO230, PRO216 or PRO302 polypeptide or detecting the presence/absence of the polypeptide is useful for diagnosis of cardiovascular, endothelial or angiogenic disorders in mammals. Anti-PRO230, PRO216 or PRO302 antibodies are useful in these diagnostic methods. The PRO230, PRO216 or PRO302 polypeptides (and their coding sequences), agonists and antagonists are useful for treatment of cardiovascular, endothelial or angiogenic disorders, especially cardiac hypertrophy (especially characterized by presence of an elevated level of Pgf-2alpha), trauma or cancer, myocardial infarction or age-related macular degeneration. In particular, PRO216, an agonist of PRO216, an antagonist of PRO230, PRO216 or PR302 or an anti-PRO216 antibody is useful for inhibition of endothelial cell growth in a mammal. Endothelial cell growth can be stimulated by administration of PRO230, a PRO230 agonist or antagonist or an anti-PRO230 antibody. Additionally, an anti-PRO302 antibody can inhibit angiogenesis induced by PRO302 in a mammal.		
XX			

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SQ      Sequence      421 AA;
Query Match      18.4%; Score 366; DB 21; Length 421;
Best Local Similarity 29.3%; Pred. No. 1.8e-25;
Matches 95; Conservative 73; Mismatches 138; Indels 18; Gaps 8;

QY      41 DDDDDDDDDDDSLFFTRPRSHFFPDLFPM-CFFGQCQ---YSRVVHCSDLGITVSP 96
D      28 DEDYDQEPDDDYQTFPPRQNVYGVFFHGYTLGCYSECFCTPNFSSMYCDNRKLKTP 87

QY      97 TNIPFTRMLDLQNNKIKEIKENDEKGLTSLYGLLIINNKL--TKIHPKAFLTTKKLRL 154
D      88 -NIPMHIQQLYQFNEIEAVTANSFINATHKEINLSHNKIKSQIDYGVFAKLPLQL 146

QY      155 YLSHNSLSEIPLNPKSLAELRIHENKVKIKQDFTKGMNALHVLMSANPLDNNIEPG 214
D      147 HLEHNNEEFPPPLPKSLERLLLYNEISKQLQTNAMDGLVNLMLDLCVNYLHDSLLKDK 206

QY      215 AFEGV-TVFHIRIAEAKLTSVPKGLPPTLLEHLDYNKISTVELEDFKRYKELQRLGLGN 273
D      207 IFAKMEKLMQLNLCNSNRLESMPPLPSSLMYLSLENNISISSIPEKYFDKLPKLTLMRSH 266

QY      274 NKITDIENGSLANIPRVREIHLNENKLLK---IPSGLPPELKYLIQIIFLHNSIARVGVND 330
D      267 NKLODIPY-NIFNLPNTVELSVGHNKLKQAFYIPRNLEHL-----YLNNEIEKMNLT 319

QY      331 FCPTVPRMKKSLVSAISLFNNPVK 354
D      320 MCPSIDPLHYHLTYIRVDQNKLK 343

RESULT 45
AAU12322
ID      AAU12322 standard; Protein; 421 AA.
AC      AAU12322;
XX      24-OCT-2001 (first entry)
XX      Human PRO216 polypeptide sequence.
XX      Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW      breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW      cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW      adipocyte; A-peptide; factor VIIA; gene therapy.
XX      Homo sapiens.
XX      WO200140466-A2.
XX      07-JUN-2001.
XX      01-DEC-2000; 2000WO-US32678.
XX      01-DEC-1999; 99WO-US28301.
XX      01-DEC-1999; 99WO-US28634.
XX      02-DEC-1999; 99WO-US28551.
XX      02-DEC-1999; 99WO-US28564.
XX      02-DEC-1999; 99WO-US28565.
XX      09-DEC-1999; 99US-0170262.
XX      16-DEC-1999; 99WO-US30095.
XX      20-DEC-1999; 99WO-US30911.
XX      20-DEC-1999; 99WO-US30999.
XX      30-DEC-1999; 99WO-US31243.
XX      06-JAN-2000; 2000WO-US00277.
XX      06-JAN-2000; 2000WO-US00376.
XX      11-FEB-2000; 2000WO-US03565.
XX      18-FEB-2000; 2000WO-US04341.
XX      18-FEB-2000; 2000WO-US04342.
XX      22-FEB-2000; 2000WO-US04414.
XX      24-FEB-2000; 2000WO-US04914.
XX      24-FEB-2000; 2000WO-US05004.
XX      01-MAR-2000; 2000WO-US05601.

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PR      20-MAR-2000; 2000WO-US07377.
PR      21-MAR-2000; 2000WO-US07532.
PR      30-MAR-2000; 2000WO-US08439.
PR      17-MAY-2000; 2000WO-US13705.
PR      22-MAY-2000; 2000WO-US14042.
PR      30-MAY-2000; 2000WO-US14941.
PR      02-JUN-2000; 2000WO-US15284.
PR      10-NOV-2000; 2000WO-US0873.
XX      (GETH ) GENENTECH INC.
XX      Baker KP, Beresini M, Deforge L, Desnoyers L, Fillaroff E, Gao W;
PI      Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI      Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX      WPI; 2001-408281/43.
XX      N-PSDB; AAS21394.
XX      Isolated, secretory and transmembrane PRO polypeptide used to detect
PT      other PRO polypeptides, link bioactive molecules to cells expressing
PT      PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT      lung, breast, prostate, cervical
XX      Claim 12; Fig 302; 813pp; English.
XX      AAU12172-AAU12446 represent novel human secretory and transmembrane
CC      PRO polypeptides. The PRO polypeptides are useful to detect other
CC      PRO polypeptides, to link bioactive molecules to cells expressing
CC      PRO polypeptides, to modulate biological activities of cells expressing
CC      PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC      breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC      polypeptide expression in a cell sample to that in a control sample.
CC      Some of the 275 sequences are also useful to stimulate the release of
CC      tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC      proliferation or differentiation of chondrocytes, the proliferation or
CC      gene expression in pericyte cells, the release of proteoglycans from
CC      cartilage, the proliferation of inner ear utricular supporting cells or
CC      of T-lymphocytes, the release of a cytokine from peripheral blood
CC      monocytes (PBMCs), or the proliferation of endothelial cells. Some of
CC      the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC      skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC      to factor VIIA. The PRO polypeptides can be used in assays to identify
CC      molecules involved in binding interactions. The polynucleotides encoding
CC      PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC      transgenic or knock out animals and can be used in gene therapy.
XX      Sequence 421 AA;
SQ      Query Match      18.4%; Score 366; DB 22; Length 421;
          Best Local Similarity 29.3%; Pred. No. 1.8e-25;
          Matches 95; Conservative 73; Mismatches 138; Indels 18; Gaps 8;

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CC sclerosis, diabetes and arthritis, viral and bacterial infections,  
 CC allergies and blood coagulation disorders. The present sequence is a  
 CC protein of the invention.  
 XX  
 SQ Sequence 772 AA;

Query Match 18.4%; Score 366; DB 22; Length 772;  
 Best Local Similarity 29.3%; Pred. No. 4.3e-25;  
 Matches 95; Conservative 73; Mismatches 138; Indels 18; Gaps 8;

QY 41 DDDDDDDDDDDNSLFPPTREPSRHHFPDLPFM-CPFGCQC---YSRVVHCSDLGLTSVP 96  
 Db 379 DEDYDQEPDDDDYQTGFPRQNDYGVFPFHTGLGCVSECFCTNPPSSMYCDNRKLTIP 438  
 QY 97 TWNPDTMLDQNNKIKELKENDPKGLTSLYGLTLNNKL--TKIHPKALTTTKLRL 154  
 Db 439 -NIPMHIOOLYLOFNEIEAVTANSINATHKEINLSNKKIKSOKIDYGVFAKLPNLLQ 497  
 QY 155 YLSHNSLSEIPLNPKSLAELRIHENKVKIKQDTFGKGMNALHVLMSANPLDNNGIEPG 214  
 Db 498 HLEHNNEEPFPLPKSLERLLGYNYSIKLTQTNAMDGLVNLTMLDLCYNVHDSLLKDX 557  
 QY 215 AFEVGV-TYFHTRIAKATSVKPLPLLELHLDYNNKISTVELEDFKRYKELQRLGNG 273  
 Db 558 IFAPKEKLMQMLCSNRLESMPGLPSSLMYLSLENNSSISSTPEKYPFKLPKLTLM 617  
 QY 274 NKITDIENGSLANIPRVREIHLNNKLLK---IPSGLPKALYLOIIFLHNSIARVGVND 330  
 Db 618 NKLODIPY-NFNLNPNIVELSVGHKLLKQAFYIPNLEHL-----YLQNNNEIEKMLTV 670  
 QY 331 FCTVPKMKKSLYSALSIFNPNVK 354  
 Db 671 MCPSIDPLHYHHLTYIRVDQNK 694

RESULT 49  
 AAM40226  
 ID AAM40226 standard; Protein; 674 AA.  
 AC AAM40226;  
 XX  
 DT 22-OCT-2001 (first entry)  
 DE Human polypeptide SEQ ID NO 3371.  
 XX  
 KW Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200153312-A1.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 26-DEC-2000; 2000WO-US34263.  
 XX  
 PR 21-JAN-2000; 2000US-0488725.  
 PR 25-APR-2000; 2000US-0552317.  
 PR 09-JUL-2000; 2000US-0598042.  
 PR 19-JUL-2000; 2000US-0620312.  
 PR 03-AUG-2000; 2000US-0653450.  
 PR 14-SEP-2000; 2000US-0662191.  
 PR 19-OCT-2000; 2000US-0693036.  
 PR 29-NOV-2000; 2000US-0727344.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
 XX  
 DR WPI; 2001-442253/47.  
 DR N-PSDB; AA159382.  
 XX  
 PT Novel nucleic acids and polypeptides, useful for treating disorders  
 PT such as central nervous system injuries -  
 XX  
 PS Example 5; SEQ ID NO 3371; 10078pp; English.  
 XX  
 CC The invention relates to human nucleic acids (AA157798-AA161369) and  
 CC the encoded polypeptides (AAM38642-AAM42213) with neurotropic,  
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localised neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: immune system suppression,  
 CC Actin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemias and  
 CC C.N.S disorders.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification.  
 XX  
 SQ Sequence 674 AA;

Query Match 18.2%; Score 363.5; DB 22; Length 674;  
 Best Local Similarity 32.7%; Pred. No. 6e-25;  
 Matches 92; Conservative 51; Mismatches 105; Indels 33; Gaps 7;

QY 74 CPFGCCYSRVVHCSDLGLTSVPTNPFDTRMLDQNNKIKELKENDFKGLTSLYGLILN 133  
 Db 54 CPSCVCRDNGFIYCNDRGLTSIPADIPDDATTLYLQNNQI-----N 94  
 QY 134 NNKLTIKHPKAFITTKRLRLYLHNSQLSEIPLNPKSLAELRIHENKVKKIQKDTFKGM 193  
 Db 95 NAGI-----PODLTKVNVQVIYLYENDLDEFINLPSRELHLDQNNVTRTARDSIARI 150  
 QY 194 NALHVLMSANPLDNNNGIEPGAF-EGVTVFHRIAEAKLTSVPKGLPPTLLELHLDYNKI 252  
 Db 151 PLEKLEHLDNNSVTSVSIEDAFADSKQLKLLFSLRNHLSIPSGLPHTLEELRLDDNRI 210  
 QY 253 STVELEDFKRYKELQRLGNNKITD--TENGSLANIPRVREIHLNNKIKKIPSGLP 310  
 Db 211 STIPLHAFKGLNSRLRLVLDGNLLAQRIADDFSLQNLTELSELVRSNLAAPPLNPS- 269  
 QY 311 KYLQIIFLHNSIARVGVNDFCTVPKMKKSLYSALSIFNN 351  
 Db 270 AHLQKLYLDQNAISHIPYN---TLAKMRE--LERLDLSNN 304

RESULT 50  
 AAU12189  
 ID AAU12189 standard; Protein; 674 AA.  
 XX  
 AC AAU12189;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Human PRO1483 polypeptide sequence.  
 XX  
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;  
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;  
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;  
 KW adipocyte; A-peptide; factor VIIA; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200140466-A2.  
 XX

PD 07-JUN-2001.  
 XX 01-DEC-2000; 2000WO-US32678.  
 XX 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 09-DEC-1999; 99US-0170262.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 20-DEC-1999; 99WO-US30999.  
 PR 30-DEC-1999; 99WO-US31243.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 01-MAR-2000; 2000WO-US05601.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 10-NOV-2000; 2000WO-US30873.  
 XX (GETH ) GENENTECH INC.

XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI; 2001-408281/43.  
 DR N-PSDB; AAS21261.

XX Isolated, secretory and transmembrane PRO polypeptide used to detect  
 PT other PRO polypeptides, link bioactive molecules to cells expressing  
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.  
 PT lung, breast, prostate, cervical

PS Claim 12; Fig 36; 813pp; English.

XX AAU12172-AAU12446 represent novel human secretory and transmembrane  
 CC PRO polypeptides. The PRO polypeptides are useful to detect other  
 CC PRO polypeptides, to link bioactive molecules to cells expressing  
 CC PRO polypeptides, to modulate biological activities of cells expressing  
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,  
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
 CC polypeptide expression in a cell sample to that in a control sample.  
 CC Some of the 275 sequences are also useful to stimulate the release of  
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the  
 CC proliferation or differentiation of chondrocytes, the proliferation or  
 CC gene expression in pericyte cells, the release of proteoglycans from  
 CC cartilage, the proliferation of inner ear utricular supporting cells or  
 CC of T-lymphocytes, the release of a cytokine from peripheral blood  
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of  
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by  
 CC skeletal muscle cells or adipocytes; or inhibit binding of A-peptide  
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify  
 CC molecules involved in binding interactions. The polynucleotides encoding  
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,  
 CC transgenic or knock out animals and can be used in gene therapy.

XX Sequence 674 AA;

Query Match 18.2%; Score 363.5; DB 22; Length 674;  
 Best Local Similarity 32.7%; Pred. No. 6e-25;

	Matches	92; Conservative	51; Mismatches	105; Indels	33; Gaps	7;
QY 74	CPEGCOCYSRVVHCSDGLTSTPTNIPFTRMLDQNNKKEIKENDEKGLTSLYGLILN	133				
Db 54	CPSVCRCDNGFIYCNDRGLTSPADIPDDATTLYLQNNQI-----N	94				
QY 134	NNKLTAKIHPKAFITTKKRLRLYLSHNOISEIPNLNPKSLAELRIHENKVKIKQKDTFKGM	193				
Db 95	NAGI-----PQDLKTKVNVQVIYENDLDEFFINLPRSLRELHLQDNNVVRTIARDSLARI	150				
QY 194	NALHVLEMSANPLDNNNGIEPGAF-EGVTTFVHFIRIAEAKLTSVPGKLPPTLLLEHLHDYNKI	252				
Db 151	PLELEKHLDDNSVSTVSIIEEDAFADSKQLLFLSRNHLSSIPSGLPHTLEELRDLDDNKI	210				
QY 253	STVELEDFKRYKELQRLGLGNNKITD--LENGSLANIPRVREIHLNKKKKIPSGLP	310				
Db 211	STIPLHAFKGLNSLRRLVLDGNLANQRIADDTFSRLQNLTELSLVRSNLAAPPLNLP-	269				
QY 311	KYLQIIFLHNSIARVGVNDPCTVPKMKKSLYSALSLENN	351				
Db 270	AHLQKLYLQDNAISHIPYN---TLAKMRE--LERLDLSNN	304				

Search completed: January 24, 2003, 12:25:34  
 Job time : 42 secs





QY 301 KKIPSGLPKLYLOIIFLHNSIARVGNDFCPTVPKMKKSLYSALSIFNPNPKYWEWOP 360  
 DB 295 KKIPSGLPKLYLOIIFLHNSIARVGNDFCPTVPKMKKSLYSALSIFNPNPKYWEIOP 354  
 QY 361 ATFCVLSRMSVQLGNFG 378  
 DB 355 ATFCVLSRMSVQLGNVG 372

RESULT 2  
 US-08-303-238-3  
 : Sequence 3, Application US/08303238  
 : Patent No. 5654270  
 : GENERAL INFORMATION:  
 : APPLICANT: RUOSLAHTI, ERKKI I.  
 : APPLICANT: LONGAKER, MICHAEL T.  
 : APPLICANT: WHITBY, DAVID J.  
 : APPLICANT: HARPER, JOHN R.  
 : APPLICANT: PIERSCHBACHER, MICHAEL D.  
 : APPLICANT: BORDER, WAYNE A.  
 : TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS  
 : TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING SCARRING  
 : NUMBER OF SEQUENCES: 8  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: CAMPBELL AND FLORES  
 : STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700  
 : CITY: SAN DIEGO  
 : STATE: CALIFORNIA  
 : COUNTRY: UNITED STATES  
 : ZIP: 92122  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/303,238  
 : FILING DATE:  
 : CLASSIFICATION: 514  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/978,931  
 : FILING DATE: 17-NOV-1992  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: KONSKI, ANTOINETTE F.  
 : REGISTRATION NUMBER: 34,202  
 : REFERENCE/DOCKET NUMBER: P-LA 9453  
 : TELEPHONE: 619-535-9001  
 : TELEFAX: 619-535-8949  
 : INFORMATION FOR SEQ ID NO: 3:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 368 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: protein  
 : US-08-303-238-3

Query Match 51.3%; Score 1021; DB 1; Length 368;  
 Best Local Similarity 52.4%; Pred. No. 5e-93;  
 Matches 197; Conservative 64; Mismatches 95; Indels 20; Gaps 3;

QY 6 LLLFLALCSAKPF-----FSPSHIALKNNMLKDMEDTDDDDDDDDDDDDNSLFFPTREP 61  
 DB 7 LVSLALSAQALPFEQGFWDFTLDDGPFPMNDEEASGADTSGVLDPD-----SVTPTYS- 60  
 QY 62 RSHFFPDLFPMPCPGCCQSYRVHCSDLGLTSVPTNIPFTYRMLDLONNKIKEIKENDF 121  
 DB 61 -----AMCPFGCHLVRVQCSDGLGKSVKPEISPTDTLLDLQNNDISLRLKDF 110  
 QY 122 KGLTSLYGLILANNKLTIKTHPAFLTTKKRLYLHNSHOLSEIPLNLPKSLAELRIHENK 181  
 DB 111 KGLQHLVALVLYNNKISKIHEKAFSPLRNVQKLYISKNLHVEIIPNLPSSLVELRHONR 170

QY 182 VKKIOKDTFKGMALHVLHNSANPLDNNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPT 241  
 DB 171 IRKVPNGVPSGLRNNNCIDMGNGPLENSGFEPGADGLKLNLYLRISAKLTGIPKDLPET 230  
 QY 242 LLELHLDYNNKISTVELEDFKRYKELQRLGLGNKKTIDTENGSLANIPIVREIHLNNKIK 301  
 DB 231 LNELHLDHNNKIOAIELEDLRYSKLYRLGLGHNQIRMIENGSLSPFTLREIHLNKKLA 290  
 QY 302 KIPSGLPKLYLOIIFLHNSIARVGNDFCPTVPKMKKSLYSALSIFNPNPKYWEWOP 361  
 DB 291 RYPSGLPDLKLLQVYVLYHNSNITKVCVNDPCPWGFGVKRAYNGISLNFNPNPYWEVOP 350  
 QY 362 TFCVLSRMSVQLGNF 377  
 DB 351 TFCVTDRLAIQFGNY 366

RESULT 3  
 US-08-458-834-3  
 : Sequence 3, Application US/08458834  
 : Patent No. 6277812  
 : GENERAL INFORMATION:  
 : APPLICANT: RUOSLAHTI, ERKKI I.  
 : APPLICANT: LONGAKER, MICHAEL T.  
 : APPLICANT: WHITBY, DAVID J.  
 : APPLICANT: HARPER, JOHN R.  
 : APPLICANT: PIERSCHBACHER, MICHAEL D.  
 : APPLICANT: BORDER, WAYNE A.  
 : TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS  
 : TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING SCARRING  
 : NUMBER OF SEQUENCES: 8  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: CAMPBELL AND FLORES  
 : STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700  
 : CITY: SAN DIEGO  
 : STATE: CALIFORNIA  
 : COUNTRY: UNITED STATES  
 : ZIP: 92122  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/458,834  
 : FILING DATE:  
 : CLASSIFICATION: 514  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/978,931  
 : FILING DATE: 17-NOV-1992  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: KONSKI, ANTOINETTE F.  
 : REGISTRATION NUMBER: 34,202  
 : REFERENCE/DOCKET NUMBER: P-LA 9453  
 : TELEPHONE: 619-535-9001  
 : TELEFAX: 619-535-8949  
 : INFORMATION FOR SEQ ID NO: 3:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 368 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: protein  
 : US-08-458-834-3

Query Match 51.3%; Score 1021; DB 4; Length 368;  
 Best Local Similarity 52.4%; Pred. No. 5e-93;  
 Matches 197; Conservative 64; Mismatches 95; Indels 20; Gaps 3;

QY 6 LLLFLALCSAKPF-----FSPSHIALKNNMLKDMEDTDDDDDDDDDDDDNSLFFPTREP 61  
 DB 7 LVSLALSAQALPFEQGFWDFTLDDGPFPMNDEEASGADTSGVLDPD-----SVTPTYS- 60

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QY 62 RSHFPFDLPMPGCGOCYSRVVHCSDLGLTSVPTNIPEDTRMLDLQNNKIKETKENDF 121
Db 61 -----AMCPGCHLRVVOCSDLGLKSVPEISPDFTLLDQNNDISELRKDDF 110
QY 122 KGLTSLYGLILNNKLTIKHPKAFITTKKRLRLYLSHNQLSEIPLNLPKSLAEIRIHENK 181
Db 111 KGLQHLALVNLNKKISKIHEKAFSPLRNVQKLYISKHNLVEIPNLPSSSLVELRIHNR 170
QY 182 VKKIQDFTKGNALHVLMSANPLDNGIEPGAFEGVTVPHIRIAEAKLTSVPKGLPPT 241
Db 171 IRKVPNGVFSGLRNNMCITEMGNPLENSGFEGAFDGLKLYLRISAEAKLTGIPKDLPET 230
QY 242 LLELHLDYNKISTVELEDFKRYKEQLRQLGLGNKKTIDTENGSLANIPRVREIHLNKKLK 301
Db 231 LNELHLDHKNKIOALEDLRLRYSKLYRLGLGHQIRMTENGSLFPLTRELHLDNNKLA 290
QY 302 KIPSGLPKLYLOIIFLHNSNITKVGNDFCPTVPMKKSLSAISLNNPVKYWEQPA 361
Db 291 RVPISGLPDLKLVVYLHNSNITKVGNDFCPTMGFGVKRAYNGISLNNPVKYWEQPA 350
QY 362 TPRCVLSRMSVOLGNF 377
Db 351 TPRCVTDRLAIQFGNY 366

```

## RESULT 4

5340934-2

; Patent No. 5340934

; ROBEY, PAMELA G.

; TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS

; NUMBER OF SEQUENCES: 13

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/432,044

; FILING DATE: 03-NOV-1989

; SEQ ID NO: 2

; LENGTH: 368

5340934-2

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Query Match 51.2%; Score 1020; DB 6; Length 368;
Best Local Similarity 52.1%; Pred. No. 6.3e-93;
Matches 196; Conservative 66; Mismatches 94; Indels 20; Gaps 3;

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QY 6 LILFLALCSAKPF----FSPSHIALKNMMLKDMEDTDDDDDDDDDDDDSDNSLFPPTREP 61
Db 7 LVSLALSAQAPFEQGEWDFTLDDGPFMMNDEASGADTSGVLDPD-----SVTPYS- 60
QY 62 RSHFPFDLPMPGCGOCYSRVVHCSDLGLTSVPTNIPEDTRMLDLQNNKIKETKENDF 121
Db 61 -----AMCPGCHLRVVOCSDLGLKSVPEISPDFTLLDQNNDISELRKDDF 110
QY 122 KGLTSLYGLILNNKLTIKHPKAFITTKKRLRLYLSHNQLSEIPLNLPKSLAEIRIHENK 181
Db 111 KGLQHLALVNLNKKISKIHEKAFSPLRNVQKLYISKHNLVEIPNLPSSSLVELRIHNR 170
QY 182 VKKIQDFTKGNALHVLMSANPLDNGIEPGAFEGVTVPHIRIAEAKLTSVPKGLPPT 241
Db 171 IRKVPNGVFSGLRNNMCITEMGNPLENSGFEGAFDGLKLYLRISAEAKLTGIPKDLPET 230
QY 242 LLELHLDYNKISTVELEDFKRYKEQLRQLGLGNKKTIDTENGSLANIPRVREIHLNKKLK 301
Db 231 LNELHLDHKNKIOALEDLRLRYSKLYRLGLGHQIRMTENGSLFPLTRELHLDNNKLA 290
QY 302 KIPSGLPKLYLOIIFLHNSNITKVGNDFCPTVPMKKSLSAISLNNPVKYWEQPA 361
Db 291 RVPISGLPDLKLVVYLHNSNITKVGNDFCPTMGFGVKRAYNGISLNNPVKYWEQPA 350
QY 362 TPRCVLSRMSVOLGNF 377
Db 351 TPRCVTDRLAIQFGNY 366

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## RESULT 5

US-08-303-238-4

; Sequence 4, Application US/08303238

; Patent No. 5654270

; GENERAL INFORMATION:

; APPLICANT: RUOSLAHTI, ERKKI I.

; APPLICANT: LONGAKER, MICHAEL T.

; APPLICANT: WHITBY, DAVID J.

; APPLICANT: HARPER, JOHN R.

; APPLICANT: PIERSCHBACHER, MICHAEL D.

; APPLICANT: BORDER, WAYNE A.

; TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CAMPBELL AND FLORES

; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700

; CITY: SAN DIEGO

; STATE: CALIFORNIA

; COUNTRY: UNITED STATES

; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/303,238

; FILING DATE:

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/978,931

; FILING DATE: 17-NOV-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: KONSKI, ANTOINETTE F.

; REGISTRATION NUMBER: 34,202

; REFERENCE/DOCKET NUMBER: P-LA 9453

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619-535-9001

; TELEFAX: 619-535-8949

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 359 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-303-238-4

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Query Match 48.4%; Score 963.5; DB 1; Length 359;
Best Local Similarity 50.4%; Pred. No. 2.4e-87;
Matches 191; Conservative 65; Mismatches 100; Indels 23; Gaps 4;

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QY 1 MKEYVLLFLALCS-AKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDSDNSLFPTR 59
Db 1 MKATITILLIAQVSWAGPF---QQRGLDFPMLEDEASGIGPEVPPDRD----- 45
QY 60 EPRSHPFPDLPMPGCGOCYSRVVHCSDLGLTSVPTNIPEDTRMLDLQNNKIKEN 119
Db 46 -----FEPISGVPFCRCQCHLVVVOCSDLGLDKVVKDLPPDPTLLDQNNKITEIKDG 99
QY 120 DFGLTSLYGLILNNKLTIKHPKAFITTKKRLRLYLSHNQLSEIPLNLPKSLAEIRIHE 179
Db 100 DFKNLNLHALLVNNKISKVSPCATPLVLERLYLKNQLKELPEKPKTKLOELRAHE 159
QY 180 NKVKKTKQDFTKGNALHVLMSANPLDNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGL 238
Db 160 NEITKRVKTVFNGLNQIMIVIELGTNPLKSGIENGAFQGMKLSYIRIADTNTITSPOGL 219
QY 239 PPTLLELHLDYNKISTVELEDFKRYKEQLRQLGLGNKKTIDTENGSLANIPRVREIHLN 298
Db 220 PPSLTELHLDGNKISRVDASLAKGLNLANLAKLGLSFSNLSAVDNGSLANTPHLRELHLDN 279
QY 299 KKKKIPSGLPKLYLOIIFLHNSNITKVGNDFCPTVPMKKSLSAISLNNPVKYWEM 358

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Db	160	NEITVYKVTENGUNQIVIELGTNPULKSSEINGAFQGMKKLSYIRIADNTNITSIPQGL	219
Qy	239	PPTLELHDYKNKISTVELEDFKRYKELORLGLGNKNKIIDTENGSLANIPRVREIHLENN	298
Db	220	PSLTELHDGNKISRVDASLSKLNNAKLGLSPFNSISAVDNGSLANTPHLRELHDNN	279
Qy	299	KLKKIPSGPELKYLIQIFUHSNSIARVGVNDPCPTVPKMKKLSYASISLNNPVKWEK	358
Db	280	KLTRVPGGLAEHKYIQVYVLHNNNISVVGSSDCPPGHNTKKASYSGVLSFNPQYWEI	339
Qy	359	QPATRCVLSRMSVOLGNF	377
Db	340	QPSTFRCVYVSATQLGNY	358
RESULT 7			
US-08-272-919-2			
; Sequence 2, Application US/08272919			
; Patent No. 5567807			
; GENERAL INFORMATION:			
; APPLICANT: Craig, William S.			
; APPLICANT: Harper, John R.			
; APPLICANT: Hernandez, Sam D.			
; APPLICANT: Kostel, Paul J.			
; APPLICANT: Parker, Jonathan R.			
; APPLICANT: Vedvick, Thomas S.			
; TITLE OF INVENTION: Processes for the Purification of Human			
; TITLE OF INVENTION: Recombinant Decorin and the Detection of Guanidin			
; NUMBER OF SEQUENCES: 2			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Campbell and Flores			
; STREET: 4370 La Jolla Village Drive, Suite 700			
; CITY: San Diego			
; STATE: California			
; COUNTRY: USA			
; ZIP: 92122			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patentin Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/272,919			
; FILING DATE: 08-JUL-1994			
; CLASSIFICATION: 435			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Campbell, Cathryn A.			
; REGISTRATION NUMBER: 31,815			
; REFERENCE/DOCKET NUMBER: P-LA 1040			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (619) 535-9001			
; TELEFAX: (619) 535-8949			
; INFORMATION FOR SEQ ID NO: 2:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 342 amino acids			
; TYPE: amino acid			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
US-08-272-919-2			
Query Match 47.68; Score 949; DB 1; Length 342;			
Best Local Similarity 53.94; Pred. No. 6.1e-86;			
Matches 178; Conservative 63; Mismatches 87; Indels 2; Gaps			
Qy	49	DDEDSLSFPTREPRSHFFPDLFPWCFCQCYSRVHVCSDLGLSVPTNPFTOTRMLDL	108
Db	14	EDFASIGP-EVPDDRDEPSLGPVCFRCQCHLRVVQCSDLGLDVKPDLPPDTLLDL	72
Qy	109	QNNKIKETKENDFKGLSYGLIILNNKLTIKIHPKAFLTTKLRLRYLSHNOLSEIPNL	160
Db	73	ONNKITEIKDGFKNLKNLHALIVNNKISKVSPGAFPLVKRLRYLSKNOLKELPEKM	133

QY 169 PKSLAELRIHENKVKIKQDKTFKGMNALHVLMSANPLDNNNGIEPGAFEGV-TVFHRIA 227  
 Db 133 PKTLOELRAHENEITKVRKVTNGLNOMIVIELCTNPLKSSGLIENGAFQGMKLSYRIA 192  
 QY 228 EAKITSVKGLPPTLEHLDYNKISTVELEDFKRYKELQRLGIGNNKITDIENGSLANI 287  
 Db 193 DTNITSPQGLPPTLEHLDYNKISRDVAASLKGLNNLAKLGLSFNSISAVDNGSLANT 252  
 QY 288 PRVREIHLNNKLAIFSGLPKELQLOIIFLHNSIARVGVNDPCTVPKMKKLSYSAIS 347  
 Db 253 PHLRELHLDNNKLRVPGGLAEHKYIQVYVYLNHNNSISVVGSSDFCPPGHNTKASYSYGS 312  
 QY 348 LFNNPVKYWEMQATFRCVLSRMSVOLGNF 377  
 Db 313 LFSNPVQYWEIQPSTFRVCYVRSALQNGY 342

RESULT 8  
 US-08-619-916-2  
 ; Sequence 2, Application US/08619916  
 ; Patent No. 5763276  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Craig, William S.  
 ; APPLICANT: Harper, John R.  
 ; APPLICANT: Hernandez, Sam D.  
 ; APPLICANT: Kostel, Paul J.  
 ; APPLICANT: Parker, Jonathan R.  
 ; APPLICANT: Vedvick, Thomas S.  
 ; TITLE OF INVENTION: Processes for the Purification of Human  
 ; TITLE OF INVENTION: Recombinant Decorin and the Detection of Guanidinium Ions  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Campbell and Flores  
 ; STREET: 4370 La Jolla Village Drive, Suite 700  
 ; CITY: San Diego  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 92122  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/619,916  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/272,919  
 ; FILING DATE: 08-JUL-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Campbell, Cathryn A.  
 ; REGISTRATION NUMBER: 31,815  
 ; REFERENCE/DOCKET NUMBER: P-LA 1040  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (619) 535-9001  
 ; TELEFAX: (619) 535-8949  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 342 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-619-916-2

Query Match 47.6%; Score 949; DB 1; Length 342;  
 Best Local Similarity 53.9%; Pred. No. 6,1e-86;  
 Matches 178; Conservative 63; Mismatches 87; Indels 2; Gaps 2;

QY 49 DDEDSLFPTRPRSHFFPDLPMPGFCQCYSRVHCSDGLGTSVPTNIPDTRMLDL 108  
 Db 14 EDEASGIGP-EVDDRDPEPSLGPVCPFRCCOCHLRVQCSDGLGDKVDPKDLPPDPTLLDL 72

QY 109 QNNKIKEIKENDFKGLTSLYGLILANNKLTKIHPKAFITTKLRLYLSHNSQLSEIPLNL 168  
 Db 73 QNNKITEIKDGFKNLKNLHALLVNNKISKVSPGAFPLVLERLYLSKNQLKELPEKM 132  
 QY 169 PKSLAELRIHENKVKIKQDKTFKGMNALHVLMSANPLDNNNGIEPGAFEGV-TVFHRIA 227  
 Db 133 PKTLOELRAHENEITKVRKVTNGLNOMIVIELCTNPLKSSGLIENGAFQGMKLSYRIA 192  
 QY 228 EAKITSVKGLPPTLEHLDYNKISTVELEDFKRYKELQRLGIGNNKITDIENGSLANI 287  
 Db 193 DTNITSPQGLPPTLEHLDYNKISRDVAASLKGLNNLAKLGLSFNSISAVDNGSLANT 252  
 QY 288 PRVREIHLNNKLAIFSGLPKELQLOIIFLHNSIARVGVNDPCTVPKMKKLSYSAIS 347  
 Db 253 PHLRELHLDNNKLRVPGGLAEHKYIQVYVYLNHNNSISVVGSSDFCPPGHNTKASYSYGS 312  
 QY 348 LFNNPVKYWEMQATFRCVLSRMSVOLGNF 377  
 Db 313 LFSNPVQYWEIQPSTFRVCYVRSALQNGY 342

RESULT 9  
 PCT-US95-08542-2  
 ; Sequence 2, Application PC/TUS9508542  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Jolla Cancer Research Foundation  
 ; TITLE OF INVENTION: Processes for the Purification of  
 ; TITLE OF INVENTION: Human  
 ; TITLE OF INVENTION: Recombinant Decorin and the Detection of Guanidinium  
 ; TITLE OF INVENTION: Ions  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Campbell and Flores  
 ; STREET: 4370 La Jolla Village Drive, Suite 700  
 ; CITY: San Diego  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 92122  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/08542  
 ; FILING DATE: 07-JUL-1995  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Perkins, Susan M.  
 ; REGISTRATION NUMBER: 36,405  
 ; REFERENCE/DOCKET NUMBER: FP-LA 1751  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (619) 535-9001  
 ; TELEFAX: (619) 535-8949  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 342 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; PCT-US95-08542-2

Query Match 47.6%; Score 949; DB 5; Length 342;  
 Best Local Similarity 53.9%; Pred. No. 6,1e-86;  
 Matches 178; Conservative 63; Mismatches 87; Indels 2; Gaps 2;

QY 49 DDEDSLFPTRPRSHFFPDLPMPGFCQCYSRVHCSDGLGTSVPTNIPDTRMLDL 108  
 Db 14 EDEASGIGP-EVDDRDPEPSLGPVCPFRCCOCHLRVQCSDGLGDKVDPKDLPPDPTLLDL 72  
 QY 109 QNNKIKEIKENDFKGLTSLYGLILANNKLTKIHPKAFITTKLRLYLSHNSQLSEIPLNL 168  
 Db 73 QNNKITEIKDGFKNLKNLHALLVNNKISKVSPGAFPLVLERLYLSKNQLKELPEKM 132

QY 169 PKSLAELRIHENKVKKIQKDTFGKGMNALHVLMSANPLDNNNGIEPGEVGV-TVFHIRIA 227  
 Db 133 PKTLOELRAHENEITKRVKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKLSYRIA 192  
 QY 228 EAKLTSVPGKLPPTLLEHLHDYKISTVELEDFKRYKELQRLGLGNKNTIDTENGSLANI 287  
 Db 193 DFNITSIPQGLPPSLTEHLHDGKISRVDAAASLKLGNLAKLGLSFNSISAVDNGSLANT 252  
 QY 288 PRVREIHLNENKLIKIPSGLPKLYLOIFLHNSIARVGVNDFCPTVPKMKKLSYSAIS 347  
 Db 253 PHRELHLNENKLIKIPSGLPKLYLOIFLHNSIARVGVNDFCPTVPKMKKLSYSAIS 312  
 QY 348 LFNPNVYWEQMPATFRVCLSRMSVOLGNF 377  
 Db 313 LFSNPVQWEIQPSTFRVCLSRMSVOLGNF 342  
 RESULT 10  
 US-08-442-063A-27  
 ; Sequence 27, Application US/08442063A  
 ; Patent No. 5705609  
 ; GENERAL INFORMATION:  
 ; APPLICANT: RUOSLAHTI, ERKKI I.  
 ; APPLICANT: PERSCHBACHER, MICHAEL D.  
 ; APPLICANT: CARDENAS, JOSE  
 ; APPLICANT: CRAIG, WILLIAM  
 ; APPLICANT: MULLEN, DANIEL G.  
 ; TITLE OF INVENTION: DECORIN FRAGMENTS AND METHODS OF  
 ; TITLE OF INVENTION: INHIBITING CELL REGULATORY FACTORS  
 ; NUMBER OF SEQUENCES: 62  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CAMPBELL AND FLORES  
 ; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700  
 ; CITY: SAN DIEGO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: UNITED STATES  
 ; ZIP: 92122  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/442,063A  
 ; FILING DATE: 16-MAY-1995  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/865,652  
 ; FILING DATE: 03-APR-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: CAMPBELL, CATHRYN A.  
 ; REGISTRATION NUMBER: 31,815  
 ; REFERENCE/DOCKET NUMBER: P-LA 1454  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 619-535-9001  
 ; TELEFAX: 619-535-8949  
 ; INFORMATION FOR SEQ ID NO: 27:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 333 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-442-063A-27

Query Match 47.5%; Score 947; DB 1; Length 333;  
 Best Local Similarity 54.1%; Pred. No. 9.3e-86;  
 Matches 178; Conservative 62; Mismatches 87; Indels 2; Gaps 2;  
 QY 50 DEDNSLPTREPRSHFFDFLPMCPGCCQYSRVHCSDLGITSVPTNPTFTRMLDLQ 109  
 Db 3 DEASIGP-EVPPDRDFEPLSGVPCRCQCHLRVWQSDLGDKVPKDPDPTLLDLQ 61

QY 110 NNKIKETKENDPKGLTSLYGLILNNKLTIKHPKAFLLTKKRLRLYLSHNOLSEPLNLP 169  
 Db 62 NNKITEIKODCFKLNKLNHALILVNNKISKVSPGATPLVKLERLYLSKNQKLEPKMP 121  
 QY 170 KSLAELRIHENKVKKIQKDTFGKGMNALHVLMSANPLDNNNGIEPGEVGV-TVFHIRIAE 228  
 Db 122 KTLQELRAHENEITKRVKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKLSYRIA 181  
 QY 229 AKLTSVPGKLPPTLLEHLHDYKISTVELEDFKRYKELQRLGLGNKNTIDTENGSLANI 288  
 Db 182 TMTISIPQGLPPSLTEHLHDGKISRVDAAASLKLGNLAKLGLSFNSISAVDNGSLANT 241  
 QY 289 RVREIHLNENKLIKIPSGLPKLYLOIFLHNSIARVGVNDFCPTVPKMKKLSYSAIS 348  
 Db 242 HLRELHLNENKLIKIPSGLPKLYLOIFLHNSIARVGVNDFCPTVPKMKKLSYSAIS 301  
 QY 349 FNNPVYWEQMPATFRVCLSRMSVOLGNF 377  
 Db 302 FSNPVQWEIQPSTFRVCLSRMSVOLGNF 330  
 RESULT 11  
 5340934-4  
 ; Patent No. 5340934  
 ; APPLICANT: TERMINE, JOHN D.; YOUNG, MARIAN F.; FISHER, LARRY W.  
 ; ROBEY, PAMELA G.  
 ; TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS  
 ; NUMBER OF SEQUENCES: 13  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/432,044  
 ; FILING DATE: 03-NOV-1989  
 ; SEQ ID NO: 4  
 ; LENGTH: 353  
 ; 5340934-4  
 Query Match 45.5%; Score 907; DB 6; Length 353;  
 Best Local Similarity 49.1%; Pred. No. 9.4e-82;  
 Matches 183; Conservative 61; Mismatches 107; Indels 22; Gaps 3;  
 QY 6 LLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDDDDDD 65  
 Db 1 LLLLAQVSWAGPF--QQKGLDFDLEDEASGIGPEVDDRD----- 39  
 QY 66 FPDFLPMCPGCCQYSRVHCSDLGITSVPTNPTFTRMLDLQNNKIKEIKENDPKGLT 125  
 Db 40 FEPGLPVCPCRCQCHLRVWQSDLGDKVPKDPDPTLLDLQNNKITEIKDGFKNK 99  
 QY 126 SLYGLILNNKLTIKHPKAFLLTKKRLRLYLSHNOLSEPLNPKSLAELRIHENKVKKI 185  
 Db 100 NLHALILVNNKISKVSPGATPLVKLERLYLSKNQKLEPKMPKTLQELRAHENEITKV 159  
 QY 186 QKDTFGKGMNALHVLMSANPLDNNNGIEPGEVGV-TVFHIRIAEAKLTSVPGKLPPTLLE 244  
 Db 160 KAVTENGLOMIVIELGTNPLKSSGIENGAFQGMKLSYRIA 219  
 QY 245 LHLDYNKISTVELEDFKRYKELQRLGLGNKNTIDTENGSLANI 304  
 Db 220 LHLDNKISRVDAAASLKLGNLAKLGLSFNSISAVDNGSLANT 279  
 QY 305 SGLPELKYLOIFLHNSIARVGVNDFCPTVPKMKKLSYSAISLFPNPNVYWEQMPATFR 364  
 Db 280 GGLAEHKYIOVVYLLHNNNISVVGSSDFCPGHNTKKASYGSVLSFNPVQWEIQPSTFR 339  
 QY 365 CVLSRMSVOLGNF 377  
 Db 340 CVVRSALQGNF 352  
 RESULT 12  
 US-08-442-063A-48  
 ; Sequence 48, Application US/08442063A  
 ; Patent No. 5705609  
 ; GENERAL INFORMATION:



```

; Patent No. 5705609
; GENERAL INFORMATION:
; APPLICANT: RUOSLAHTI, ERKKI I.
; APPLICANT: PIERSCHBACHER, MICHAEL D.
; APPLICANT: CARDENAS, JOSE
; APPLICANT: CRAIG, WILLIAM
; APPLICANT: MULLEN, DANIEL G.
; TITLE OF INVENTION: DECORIN FRAGMENT'S AND METHODS OF
; TITLE OF INVENTION: INHIBITING CELL REGULATORY FACTORS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,063A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: US 07/865,652
; FILING DATE: 03-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 1454
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-442-063A-42

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Query Match 30.9%; Score 616; DB 1; Length 236;
Best Local Similarity 52.4%; Pred. No. 3.6e-53;
Matches 122; Conservative 40; Mismatches 69; Indels 2; Gaps 2;

QY 50 DEDNSLPTPREPSHFFPDLFPMCPGQCYSRVVHCHSDGLTSVPTNIPFDTMLDLQ 109
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3 DEASGIGP-EVPDDRDFEPSLGPVCPQCCHLRVVOCSDLGLDKVPKDLPPDTLLDLQ 61

QY 110 NNKIKEIKENDFKGLTSGLYLNNKLTIKHPKAFITTKLRLRLYLSHNOLSEIPLNP 169
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 62 NNKITEIKDGFKNLKNLHALILVNNKISKVSGAFTPLVKLERLYLSKNOLKELPEKMP 121

QY 170 KSLAELRIHENKVKIKQDTFKGMNALHVLMSANPLDNNNGIEPGAEGV-TVFHIRIAE 228
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 122 KTLQELRAHENETTKVRKVTFNGLNQMVIELGTNPLKSSGIENGAFQGMKKLSYRIAD 181

QY 229 AKLTSVPGKLPPLLEHLHDYKISTVELEDFKRYKELQRLGLGNKKITDIEN 281
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 182 TNITSIPOGLPPLSELHLHDGKNISRVDAASLKLNLNLAKLGLSFNSISAVDN 234

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RESULT 15
US-08-442-063A-39
; Sequence 39, Application US/08442063A
; Patent No. 5705609
; GENERAL INFORMATION:
; APPLICANT: RUOSLAHTI, ERKKI I.
; APPLICANT: PIERSCHBACHER, MICHAEL D.
; APPLICANT: CARDENAS, JOSE

```

```

; APPLICANT: CRAIG, WILLIAM
; APPLICANT: MULLEN, DANIEL G.
; TITLE OF INVENTION: DECORIN FRAGMENTS AND METHODS OF
; TITLE OF INVENTION: INHIBITING CELL REGULATORY FACTORS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,063A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: US 07/865,652
; FILING DATE: 03-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 1454
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-442-063A-39

Query Match 24.7%; Score 493; DB 1; Length 188;
Best Local Similarity 53.0%; Pred. No. 4e-41;
Matches 98; Conservative 32; Mismatches 53; Indels 2; Gaps 2;

QY 50 DEDNSLPTPREPSHFFPDLFPMCPGQCYSRVVHCHSDGLTSVPTNIPFDTMLDLQ 109
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3 DEASGIGP-EVPDDRDFEPSLGPVCPQCCHLRVVOCSDLGLDKVPKDLPPDTLLDLQ 61

QY 110 NNKIKEIKENDFKGLTSGLYLNNKLTIKHPKAFITTKLRLRLYLSHNOLSEIPLNP 169
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 62 NNKITEIKDGFKNLKNLHALILVNNKISKVSGAFTPLVKLERLYLSKNOLKELPEKMP 121

QY 170 KSLAELRIHENKVKIKQDTFKGMNALHVLMSANPLDNNNGIEPGAEGV-TVFHIRIAE 228
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 122 KTLQELRAHENETTKVRKVTFNGLNQMVIELGTNPLKSSGIENGAFQGMKKLSYRIAD 181

QY 229 AKLTS 233
  |||
Db 182 TNITS 186

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RESULT 16
US-08-442-063A-36
; Sequence 36, Application US/08442063A
; Patent No. 5705609
; GENERAL INFORMATION:
; APPLICANT: RUOSLAHTI, ERKKI I.
; APPLICANT: PIERSCHBACHER, MICHAEL D.
; APPLICANT: CARDENAS, JOSE
; APPLICANT: CRAIG, WILLIAM
; APPLICANT: MULLEN, DANIEL G.
; TITLE OF INVENTION: DECORIN FRAGMENTS AND METHODS OF
; TITLE OF INVENTION: INHIBITING CELL REGULATORY FACTORS
; NUMBER OF SEQUENCES: 62

```





; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CAMPBELL AND FLORES  
 ; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700  
 ; CITY: SAN DIEGO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: UNITED STATES  
 ; ZIP: 92122  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/458,834  
 ; FILING DATE:  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/978,931  
 ; FILING DATE: 17-NOV-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: KOSKI, ANTOINETTE F.  
 ; REGISTRATION NUMBER: 34,202  
 ; REFERENCE/DOCKET NUMBER: P-LA 9453  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 619-535-9001  
 ; TELEFAX: 619-535-8949  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 375 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-458-834-2

Query Match 17.2%; Score 342.5; DB 4; Length 375;  
 Best Local Similarity 27.7%; Pred. No. 9.2e-26;  
 Matches 103; Conservative 66; Mismatches 158; Indels 45; Gaps 13;

Qy	6	LLFLALCSAK--PFSPSHALKNMMLKOWEDTDDDDDD-----DDDDDDSDSLF-	56
Db	6	ILLAGLCLSWAQYEDSHWFQ--FLRNOQSTYDDPDYPYEPYPTGEEGPAYA	63
Qy	57	-----PTREPRSHFFFDLPFCPCQCQ---YSRVHCSDLGLTSVPTNIPFTDRLDLQ	109
Db	64	YGSPPQPEPRD-----CPQECDCPPNFTAMYCDNRNLKYLFP-VPSRMKYVYEQ	112
Qy	110	NNKIKEIKENDFKGLTSLYGLILNNKLT--KIHPKAFLLTKKLRRLYLSHNLSEIPLN	167
Db	113	NNQISSIOEGVFDNATGLLTALHGNQITSDKVGKVKFSLRHLERLYLDHNNLTRIPSP	172
Qy	168	LPKSLAEIRIHENKVKIKQDTFGMNAHVLEMSANPLDNNNGTEPGAFEGV-TVFHRI	226
Db	173	LPRLRLHLDHNOISRVPNNALEGLNLTALYLHNEIQEVG---SSMKGLRSLILLDL	229
Qy	227	ABAKLTSPVKGLPPTLLELHDYNNKISTVELEDPKRYKEIQRGLGNKKTIDENGSLA-	285
Db	230	SYNHLRKVPDGLPSALEOLYEHNNVTSVPDSYFRGSPKLLYVRLSHNSLT---NNGLAS	286
Qy	286	---NIPRVREIHLENNKLTTPSGLPKELQIIFLHNSNARVGVNDFCPTVPMKKS	342
Db	287	NTFNSSSLLELDLSYNQLQKIP---PVSTNLNLYLQGNRINEFSISFCTVVDVMNFSK	343
Qy	343	YSATSLFNPNVK 354	
Db	344	LQVQLDGNK 355	

RESULT 19  
 US-09-191-647-2  
 ; Sequence 2, Application US/09191647  
 ; Patent No. 6046015  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Goodman, Corey

; APPLICANT: Kid, Thomas  
 ; APPLICANT: Brose, Katja  
 ; APPLICANT: Tessier-Lavigne, Marc  
 ; TITLE OF INVENTION: Modulating Robo: Ligand Interactions  
 ; FILE REFERENCE: B98-031-3  
 ; CURRENT APPLICATION NUMBER: US/09/191,647  
 ; CURRENT FILING DATE: 1998-11-13  
 ; EARLIER APPLICATION NUMBER: 60/065,544  
 ; EARLIER FILING DATE: 1997-11-14  
 ; EARLIER APPLICATION NUMBER: 60/081,057  
 ; EARLIER FILING DATE: 1998-04-07  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 1525  
 ; TYPE: PRT  
 ; ORGANISM: human  
 ; US-09-191-647-2

Query Match 16.9%; Score 336; DB 3; Length 1525;  
 Best Local Similarity 26.5%; Pred. No. 3.2e-24;  
 Matches 105; Conservative 61; Mismatches 120; Indels 110; Gaps 12;

Qy	74	CPFGCQCYSRVHVHCSDLGLTSVPTNIPEDT-----RMLDL	108
Db	277	CPAACTCSNNIYDCRGKGLTEIPTNLP-ETITEIRLEONTIKVIPPGAFSPYKKLRRIDL	335
Qy	109	QNNKIKEIKENDFKGLTSLYGLILNNKLTIKIHPKAFLLTKKLRRLYLSHNLSEIPLN	168
Db	336	SNNQISEIAPDAFOGLRSLSLVLYGNKITELPKSLFEGLSLOLLLNANKINCLRYDA	395
Qy	169	PKSLAEIR---IHENKVKIKQDTFGMNAHVLEMSANP-----LDNNGIE	212
Db	396	FQDLHNLNLSLYDNKLTQIAKGTESPLRAIQTMHLAQNPFICDCHLKWLDYLTNPDE	455
Qy	213	PGA-----FEGVTYFH	223
Db	456	TSGARCTSPRLANKRIGOKSKKPRCSGTEDYRSKLSGDCDFADLACPEKCRCEGTV--	513
Qy	224	IRIAKLTSPVKGLPPTLLELHDYNNKISTVELED--FKRYKELQRLGNKKTIDENG	282
Db	514	-DCSNQKLNKIEPHIPOYTAELRLNNEFTVLEATGIFKKLPQLRKINFSNNKITDIEG	572
Qy	283	SIANIPRVREIHLENNKLT-----KIPSGLPKELQIIFLHNSNARVGVNDFCPTVPM	338
Db	573	AFEGASGVNEILLTSNRLNENVQHKMFKGLESKTL---MLRSNRITCVGNDSF-----I	623
Qy	339	KKSLYSATSLFNPNVKYEMQPAFRCVLSRMSVOL	374
Db	624	GLSSVRLSLYDNQIT--TVAPGAFDTLHSLSTLNL	657

RESULT 20  
 US-09-540-245A-2  
 ; Sequence 2, Application US/09540245A  
 ; Patent No. 6270984  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Goodman, Corey  
 ; APPLICANT: Kid, Thomas  
 ; APPLICANT: Brose, Katja  
 ; APPLICANT: Tessier-Lavigne, Marc  
 ; TITLE OF INVENTION: Modulating Robo: Ligand Interactions  
 ; FILE REFERENCE: B98-031-3  
 ; CURRENT APPLICATION NUMBER: US/09/540,245A  
 ; CURRENT FILING DATE: 2000-03-31  
 ; PRIOR APPLICATION NUMBER: 60/065,544  
 ; PRIOR FILING DATE: 1997-11-14  
 ; PRIOR APPLICATION NUMBER: 60/081,057  
 ; PRIOR FILING DATE: 1998-04-07  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 1525

226 CANNOT GET INTO FACTORY NOT VERY MANY TIMES ONLY ON VERY RARE OCCASIONS

```

; Patent No. 5654270
; GENERAL INFORMATION:
; APPLICANT: RUOSLAHTI, ERKKI I.
; APPLICANT: LONGAKER, MICHAEL T.
; APPLICANT: WHITBY, DAVID J.
; APPLICANT: HARPER, JOHN R.
; APPLICANT: PIERSCHBACHER, MICHAEL D.
; APPLICANT: BORDER, WAYNE A.
; TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS
; TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING SCARRING
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,238
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,931
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KONSKI, ANTOINETTE F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: P-LA 9453
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 376 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-303-238-1

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```

Query Match      16.0%; Score 318; DB 1; Length 376;
Best Local Similarity 26.1%; Pred. No. 2.5e-23;
Matches 86; Conservative 65; Mismatches 131; Indels 48; Gaps 9;

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QY 63 SHFFPFDLPPM-----CPFGCQC---YSRVVHCSDLG 91
DB 37 TYIDPYDPIYETPEYGYVDEGPATYGSPPDRDPCQCDPPNFLTAMYCDNRN 96
QY 92 LTSVPTNIPFTRMLDQNNKIKEIKENDKGLTSLYGLILNNKLT--KIHPKAFLTK 149
DB 97 LKYLPE-VPSRMKYVYFQNNQITSIQGVFNDATGLLWIALHGNQITSDKVGKRVFSKLR 155
QY 150 KLRLYLSHNOLSEIPLNPKSLAELRIHENKVKIKQDTFKGMNALHVLMSANPLDNN 209
DB 156 HLRLYLDDHNNLTMPGPLPSRLRELHLDHNOISRVPNNALEGLNLTALYLQHDIEQEV 215
QY 210 GIEPAGFEGV-TVFHIRIAEAKLTSPKGLPPTLLELHLDYNKISTVELEDFKRYKELQR 268
DB 216 G---SSMRGLRSLLLDLSYNHLRKVPDGLPSALEQLYMEHNNVYTPDSYFRGAPKLLY 272
QY 269 LGLGNKTTIDENGLA-----NIPRVREIHLNNKIKKIPSGLPKYLQIIFLHNSIA 324
DB 273 VRLSHNSLT---NNGLASNTFNSSSLELDLSYNOLQKIP---PVNTNLENLYLQGNRIN 326
QY 325 RVGNDECPYTPKMKKSLYSALISLFPNPKV 354
DB 327 EFSISSECTVVDVVFNSKLVQVRLDGNBEIK 356

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RESULT 24
US-08-458-834-1
; Sequence 1, Application US/08458834
; Patent No. 6277812
; GENERAL INFORMATION:
; APPLICANT: RUOSLAHTI, ERKKI I.
; APPLICANT: LONGAKER, MICHAEL T.
; APPLICANT: WHITBY, DAVID J.
; APPLICANT: HARPER, JOHN R.
; APPLICANT: PIERSCHBACHER, MICHAEL D.
; APPLICANT: BORDER, WAYNE A.
; TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS
; TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING SCARRING
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,834
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,931
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KONSKI, ANTOINETTE F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: P-LA 9453
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 376 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-458-834-1

```

```

Query Match      16.0%; Score 318; DB 4; Length 376;
Best Local Similarity 26.1%; Pred. No. 2.5e-23;
Matches 86; Conservative 65; Mismatches 131; Indels 48; Gaps 9;

```

```

QY 63 SHFFPFDLPPM-----CPFGCQC---YSRVVHCSDLG 91
DB 37 TYIDPYDPIYETPEYGYVDEGPATYGSPPDRDPCQCDPPNFLTAMYCDNRN 96
QY 92 LTSVPTNIPFTRMLDQNNKIKEIKENDKGLTSLYGLILNNKLT--KIHPKAFLTK 149
DB 97 LKYLPE-VPSRMKYVYFQNNQITSIQGVFNDATGLLWIALHGNQITSDKVGKRVFSKLR 155
QY 150 KLRLYLSHNOLSEIPLNPKSLAELRIHENKVKIKQDTFKGMNALHVLMSANPLDNN 209
DB 156 HLRLYLDDHNNLTMPGPLPSRLRELHLDHNOISRVPNNALEGLNLTALYLQHDIEQEV 215
QY 210 GIEPAGFEGV-TVFHIRIAEAKLTSPKGLPPTLLELHLDYNKISTVELEDFKRYKELQR 268
DB 216 G---SSMRGLRSLLLDLSYNHLRKVPDGLPSALEQLYMEHNNVYTPDSYFRGAPKLLY 272
QY 269 LGLGNKTTIDENGLA-----NIPRVREIHLNNKIKKIPSGLPKYLQIIFLHNSIA 324
DB 273 VRLSHNSLT---NNGLASNTFNSSSLELDLSYNOLQKIP---PVNTNLENLYLQGNRIN 326

```

```
QY 325 RVGVNDFCTVPKMKKSLYSATSLFNNPVK 354
Db 327 EFSISFCTVVDVWVNSKLVQVVRDGNK 356

RESULT 25
US-09-191-647-7
; Sequence 7, Application US/09191647
; Patent No. 6046015
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/191,647
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: 60/065,544
; EARLIER FILING DATE: 1997-11-14
; EARLIER APPLICATION NUMBER: 60/081,057
; EARLIER FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1480
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-191-647-7

Query Match 15.9%; Score 316; DB 3; Length 1480;
Best Local Similarity 25.1%; Pred. No. 3e-22;
Matches 98; Conservative 66; Mismatches 123; Indels 104; Gaps 9;

QY 74 CPFGCQCYSRVVHCSDGLTSTVPTNIPFDT-----RMLDLQ 109
Db 73 CPRVCCTGLNVDCSHRGLTSVPRKISADVERLELQGNLTVIYETDFQRLTKRLMLQLT 132
QY 110 NKKIKEIKENDFKGLTSLYGLILNNKLTTHPKAFLTTKKRLRLYLSHNOLSEIPLNLP 169
Db 133 DNQIHTIERNFQDLVSLERLDISNNVITTVGRVFKGAQSLRSLQLDNNQITCLDEHAF 192
QY 170 KSLAELRI---HENKVKIKQDTFKGMALHVLMSANPL----- 206
Db 193 KGLVELEILTNNNLTSLPHNIFGGLRLRALRSLDNPFACDCHLSWLSRFLRSATRLA 252
QY 207 -----DNNGIEPGA-----FEGTVVPHIRI 226
Db 253 PYTRCQSPSQLKQNVADLHDQEFKCSGLTEHAPMECCGAENSCPHPCRCADGI----VDC 308
QY 227 AEAKLTSPKGLPPTLLEHLHDYNKISTVELEDFKRYKELQRLGLGNKKTIDENGSLAN 286
Db 309 REKSLTSVPVTLDDTVDVRLQNFITELPPKSFSSFRRLRRIDLSNNISRIADHLSG 368
QY 287 IPRVREIHLNNKLIKPSGL-PELKYLIQIFLHNSIARVGVNDFCPTVPKMKKSLY-- 343
Db 369 LKQLTTLVLYGNKIKDLPSPGVFKGSLRLLLLNANEISCRKDAF-----RDLHSL 420
QY 344 SAISLFNPNVKYEMQATFRCVLSRMSVOL 374
Db 421 SLLSLYDNNIQ--SLANGTFDAMKSMKTIVHL 449

RESULT 26
US-09-540-153-7
; Sequence 7, Application US/09540153
; Patent No. 6270995
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,153
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/191,647
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1480
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-540-153-7
```

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QY 325 RVGVNDFCTVPKMKKSLYSATSLFNNPVK 354
Db 327 EFSISFCTVVDVWVNSKLVQVVRDGNK 356

RESULT 25
US-09-191-647-7
; Sequence 7, Application US/09191647
; Patent No. 6046015
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/191,647
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: 60/065,544
; EARLIER FILING DATE: 1997-11-14
; EARLIER APPLICATION NUMBER: 60/081,057
; EARLIER FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1480
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-191-647-7

Query Match 15.9%; Score 316; DB 3; Length 1480;
Best Local Similarity 25.1%; Pred. No. 3e-22;
Matches 98; Conservative 66; Mismatches 123; Indels 104; Gaps 9;

QY 74 CPFGCQCYSRVVHCSDGLTSTVPTNIPFDT-----RMLDLQ 109
Db 73 CPRVCCTGLNVDCSHRGLTSVPRKISADVERLELQGNLTVIYETDFQRLTKRLMLQLT 132
QY 110 NKKIKEIKENDFKGLTSLYGLILNNKLTTHPKAFLTTKKRLRLYLSHNOLSEIPLNLP 169
Db 133 DNQIHTIERNFQDLVSLERLDISNNVITTVGRVFKGAQSLRSLQLDNNQITCLDEHAF 192
QY 170 KSLAELRI---HENKVKIKQDTFKGMALHVLMSANPL----- 206
Db 193 KGLVELEILTNNNLTSLPHNIFGGLRLRALRSLDNPFACDCHLSWLSRFLRSATRLA 252
QY 207 -----DNNGIEPGA-----FEGTVVPHIRI 226
Db 253 PYTRCQSPSQLKQNVADLHDQEFKCSGLTEHAPMECCGAENSCPHPCRCADGI----VDC 308
QY 227 AEAKLTSPKGLPPTLLEHLHDYNKISTVELEDFKRYKELQRLGLGNKKTIDENGSLAN 286
Db 309 REKSLTSVPVTLDDTVDVRLQNFITELPPKSFSSFRRLRRIDLSNNISRIADHLSG 368
QY 287 IPRVREIHLNNKLIKPSGL-PELKYLIQIFLHNSIARVGVNDFCPTVPKMKKSLY-- 343
Db 369 LKQLTTLVLYGNKIKDLPSPGVFKGSLRLLLLNANEISCRKDAF-----RDLHSL 420
QY 344 SAISLFNPNVKYEMQATFRCVLSRMSVOL 374
Db 421 SLLSLYDNNIQ--SLANGTFDAMKSMKTIVHL 449

RESULT 26
US-09-540-153-7
; Sequence 7, Application US/09540153
; Patent No. 6270995
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
```

```

Query Match      15.9%; Score 316; DB 4; Length 1480;
Best Local Similarity 25.1%; Pred. No. 3e-22;
Matches 98; Conservative 66; Mismatches 123; Indels 104; Gaps 9;

QY 74 CPGCQCYSRVHCSDLGLTSVPTNIPEDT-----RMLDLQ 109
Db 73 CPRVCSCTGLNVDCSHRGTSVPRKISADVERLELQGNLTAVIYETDFQRLTKRLMLQLT 132
QY 110 NKKIKIKENDFKGLTSYGLLNNKLTTHPKAFITTKLRLRLYLSHNLSLSEIPLNLP 169
Db 133 DNOIHTIERNFSQDLVSLERLDSINNVTITVGRRVFKGAQSLRSLOLDNNQITCLDEHAF 192
QY 170 KSLAELRI---HENKVKIKQDFTFGKGMNALHVLMSANPL----- 206
Db 193 KGLVELEILTNNNNLTSLPHNIFGGLRLRLALRLSDNPFACDCHLSWLSRFLRSATRLA 252
QY 207 -----DNNGLIEPGA-----FEGVTVFHRI 226
Db 253 PYTRCQSPQLKQNVADLHDOEFKCSGLTEHAPMECGAENSCPHPCRCADGI-----VDC 308
QY 227 AEAKLTSPKGLPPTLLEHLHDYNNKISTVELEDFKRYKELQRLGLGNKKTIDIEGSLAN 286
Db 309 REKSLTSVPVTLDDTDVRLQNFITELPPKSFSSFRRLRLDLSNNNISRIADHLSG 368
QY 287 IPRVREIHLENKLLKIPSGL-PELKYLOITIFLHNSIARVGVNDFCPTVPKMKKSLY-- 343
Db 369 LKQLTTLVLYGNKIKDLPSPGVFKGLSRLLLNANEISCIRKDAF-----RDLHSL 420
QY 344 SAISLNNPVKYWEMOPATFCVLSRMSVOL 374
Db 421 SLLSLYDNNIQ--SLANGTFDAMKSMKTIVHL 449

RESULT 28
PCT-US91-09055-2
Sequence 2, Application PC/TUS9109055
GENERAL INFORMATION:
APPLICANT: Rothberg, Jonathan Marc and Artavanis-Tsakonas, Spyridon
TITLE OF INVENTION: Purified SLIT protein and Sequence Elements Thereof
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: Yale University
ADDRESS: Office of Cooperative Research
STREET: 246 Church Street
CITY: New Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06510
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/09055
FILING DATE: 19911127
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/624,135
FILING DATE: 7-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barth, Richard J.
REGISTRATION NUMBER: 28,180
REFERENCE/DOCKET NUMBER: 900964/RSB
TELEPHONE: (212) 972-1400
TELEFAX: (212) 370-1622
TELEX: 236268
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1480 amino acids
TYPE: AMINO ACIDS

```

```

; TOPOLOGY: Linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: signal sequence
; LOCATION: 1 to 36
; IDENTIFICATION METHOD: similarity to other signal
; OTHER INFORMATION: Directs Export
; NAME/KEY: Four Flank-LRR-Flank domains
; LOCATION: 37 to 910
; IDENTIFICATION METHOD: Array of Flank-LRR-Flank
; OTHER INFORMATION: mediates adhesive events
; NAME/KEY: Tandem EGF-like repeats
; LOCATION: 911 to 1150
; IDENTIFICATION METHOD: similarity to tandem EGF-like
; OTHER INFORMATION: protein-protein interactions
; NAME/KEY: 7th EGF-like repeat
; LOCATION: 1353 to 1393
; IDENTIFICATION METHOD: similarity to epidermal growth
; OTHER INFORMATION: Involvement in receptor-ligand
; NAME/KEY: Alternative splice segment
; LOCATION: 1394 to 1404
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: developmentally regulated
; NAME/KEY: COOH-terminal region
; LOCATION: 1405 to 1480
; IDENTIFICATION METHOD: experimental
; PCT-US91-09055-2

Query Match      15.9%; Score 316; DB 5; Length 1480;
Best Local Similarity 25.1%; Pred. No. 3e-22;
Matches 98; Conservative 66; Mismatches 123; Indels 104; Gaps 9;

QY 74 CPGCQCYSRVHCSDLGLTSVPTNIPEDT-----RMLDLQ 109
Db 73 CPRVCSCTGLNVDCSHRGTSVPRKISADVERLELQGNLTAVIYETDFQRLTKRLMLQLT 132
QY 110 NKKIKIKENDFKGLTSYGLLNNKLTTHPKAFITTKLRLRLYLSHNLSLSEIPLNLP 169
Db 133 DNOIHTIERNFSQDLVSLERLDSINNVTITVGRRVFKGAQSLRSLOLDNNQITCLDEHAF 192
QY 170 KSLAELRI---HENKVKIKQDFTFGKGMNALHVLMSANPL----- 206
Db 193 KGLVELEILTNNNNLTSLPHNIFGGLRLRLALRLSDNPFACDCHLSWLSRFLRSATRLA 252
QY 207 -----DNNGLIEPGA-----FEGVTVFHRI 226
Db 253 PYTRCQSPQLKQNVADLHDOEFKCSGLTEHAPMECGAENSCPHPCRCADGI-----VDC 308
QY 227 AEAKLTSPKGLPPTLLEHLHDYNNKISTVELEDFKRYKELQRLGLGNKKTIDIEGSLAN 286
Db 309 REKSLTSVPVTLDDTDVRLQNFITELPPKSFSSFRRLRLDLSNNNISRIADHLSG 368
QY 287 IPRVREIHLENKLLKIPSGL-PELKYLOITIFLHNSIARVGVNDFCPTVPKMKKSLY-- 343
Db 369 LKQLTTLVLYGNKIKDLPSPGVFKGLSRLLLNANEISCIRKDAF-----RDLHSL 420
QY 344 SAISLNNPVKYWEMOPATFCVLSRMSVOL 374
Db 421 SLLSLYDNNIQ--SLANGTFDAMKSMKTIVHL 449

RESULT 29
US-09-182-024A-5
Sequence 5, Application US/09182024A
Patent No. 6342370
GENERAL INFORMATION:
APPLICANT: Connolly, Timothy
APPLICANT: Rajput, Bhanu
TITLE OF INVENTION: Human Slit Polypeptide and Polynucleotides Encoding
TITLE OF INVENTION: Same
FILE REFERENCE: 640100-271
CURRENT APPLICATION NUMBER: US/09/182,024A
CURRENT FILING DATE: 1998-10-29

```

```

QY 74 CPGCCOCYSRVVCHSDGLGTSYPTNPFDTRMLDQNNKIKELKENDRKGLTSLYGLIILN 133
Db 34 CPTKCTCSAASVDCHGLGVRVPRGIPRAERLDDDRNNITRITKMDFAGLKNRLVHLLE 93
QY 134 NKKLTIRHPKAFITTKKRLRLSLHNSQLSEIPNLNPKS---LAELRIHENKVKYKIQDFF 190
Db 94 DNOQSVIERGAFQDLKOLERLNNKKNKQVLPELLFQSTPKLTRLDLSENOIQIPRKAF 153
QY 191 KGNALHVLHMSANLDNG---IEPGAFEG-----VTVF----- 222
Db 154 RGTIDVKNLQ-----LDNNHISCIEDGAFRALRDLEILTNNNISIRILVTSFNHMPKIR 208
QY 223 -----HIR-----TAEAK----- 230
Db 209 TLRHLSHLYCCHLAWLSDWLQRRTVCGQFTLCMAPVHLRNFENADVOKKEVVCAPHS 268
QY 231 -----LTSVPKGLPPTLLELHLDYDNKISTVELEDFK 261
Db 269 EPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPSCGIVEIRLEQNSIRAI PAGAFT 328
QY 262 RYKELQRLGLGNKNIITDIENGSLANTPRVREIHLNENKLNKKPSGLPE-LKYLOIIFLHS 320
Db 329 QYKKLRIDISKNOISDIAPDQFQKLSKTSLSLYGNKIKTEITAKGLFDGLVLSQLLLNA 388
QY 321 NSIARVGVNDPCPTVPKMKKSLYSALSLENNPVK 354
Db 389 NKINCLRVNTF-----QDLQNLNLLSLDNLKQ 416

RESULT 31
US-08-986-485-5
; Sequence 5, Application US/08986485
; Patent No. 6046030
; GENERAL INFORMATION:
; APPLICANT: WU, SHUJIAN
; APPLICANT: SWEET, RAYMOND
; APPLICANT: TRUNEH, ALEMSEGED
; TITLE OF INVENTION: A HUMAN LIG-1 HOMOLOG (HLIG-1)
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/986,485
; FILING DATE: 08-DEC-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/059,448
; FILING DATE: 22-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70264
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

```

US-08-986-485-5

```

Query Match      14.9%; Score 296; DB 3; Length 1091;
Best Local Similarity 30.1%; Pred. No. 1.8e-20;
Matches 94; Conservative 64; Mismatches 124; Indels 30; Gaps 12;

QY 74 CPGGQCVSRVHVCSDGLGTSYPTNPEDTRMLDQNNKIKKIEKENDFKGLTSYGLILN 133
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 43 CAAACTCAGNSUDCSGRGLATLPRLPSWTRSLNLSYRNLSEIDSAAPEDLTNQEYV 102
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 134 NKKLKIHPKAFLLTKKRLRLYLSHNLSEI---PLNLPKSLAEURLIHENKVKIKQDTF 190
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 103 SNELTAL-PSUGTAGSIGVVVSLFQHNKILSDVGSQLSYLSLEVLDDSSNNITEIRSCF 161
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 191 KGMNALHVLMSANPLDNGI---EPGAFEGV--TVFHIRIAEAKLTSVP--KGLP-PTLL 243
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 162 P--NGLRIRELN---LASNRISLESAGFDGLSRLTLRLSKNRTIQLPVKAFKLPRLT 216
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 244 ELHLYNKISTVELEDFRYKELQRLGLGNKKTIDTENGSLANIPRVREIHLNENKIKKI 303
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 217 QLDLNRNRIRIEGLTFQGLDSLEVLRLQNNISRLTDGAFWGLSKMHVLEHNSLVEV 276
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 304 PSG-LPELKYLIQIIFLHNSIARVGVN--DFCPTVPKMKKSLYSAISLFNNPVKYWQ 360
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 277 NSGSLYGLTALHQLHLSNNSISRIQDWSFC-----QKLHELILSFNNLTIRLDESL 329
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 361 ATFCVLSRMSV 372
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 330 AE---LSSLSI 337
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 32
US-08-190-802A-50
; Sequence 50, Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/190,802A
; FILING DATE: 01-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 8600-0139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 603 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:

```

```

; INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
; INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33
US-08-190-802A-50

Query Match      13.7%; Score 272; DB 1; Length 603;
Best Local Similarity 28.2%; Pred. No. 1.8e-18;
Matches 90; Conservative 57; Mismatches 108; Indels 64; Gaps 12;

QY 102 DTRMLDQNNKIKKIEKENDFKGLTSYGLILNKKTKTHKRAFLTKKRLRIYLSHNL 161
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 219 ELRELDLSNRALRSVAVNFVHLPRQLKLYLDRLNLTAVAPGAFGLMKALRWLDLSHNRV 278
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 162 SET-----PKS-----LAEIRIHENKVKIKQDTFKGMN 194
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 279 AGLMEDTFFCLLGLHVLRIAHNAIASLRPTFKDLHLEELQLGHNRIRQLGERTFEGLG 338
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 195 ALHVLMSANPLDNGIEPCAFEGVTVFHIRIAEAK---LTSVP-----KGLPPTLLEHL 247
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 339 QLEVLTLNDNQITE--VRVGAFGS--LFNVAVMNLSGNCLRSPLRVFQGL-DKLHSLHL 393
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 248 DYNKISTVELEDFRYKELQRLGLGNKKTIDTENGSLANIPRVREIHLNENKIKKIP--- 304
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 394 EHCIGHVRLHFTAGSLGRRLFLRDNSSISIEEQSLAGLSLELDLTNRLTHLPROL 453
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 305 -SGLPELKYLIQIIFLHNSIARVGVNDFCPT-----VPKMKKSLYSA----- 345
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 454 FQGLGHLEYL---LLSYNQLITLSAEVLGLQRAFWDISHNHLETLAGLFSLSLGRVRY 510
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 346 ISLFNNPVKYWQPATFR 364
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 511 LSLRNNSLQTFSPQGLER 529
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

```

RESULT 33
US-08-477-346-50
; Sequence 50, Application US/08477346
; Patent No. 6262023
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/477,346
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/487,072
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 603 amino acids
; TYPE: amino acid

```



;  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: Insulin-like growth factor bind.  
; INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33  
US-08-477-346-50

Query Match 13.7%; Score 272; DB 4; Length 603;  
Best Local Similarity 28.2%; Pred. No. 1.8e-18;  
Matches 90; Conservative 57; Mismatches 108; Indels 64; Gaps 12;

QY 102 DTRMLDQNNKIKKEIKENDFKGLTSLYGLILNNKLTTHPKAPLTKKLRRLYLSHNQL 161  
Db 219 ELRELDLSRNALRSVKANVFVHLPRLOKLYLDRNLITAVAPGAFGLMKALRWLDLSHNRV 278  
QY 162 SEI-----PLNL-----PKS-----LAELRIHENKVKKTKQKDTFGMN 194  
Db 279 AGLMEDTFPGLLGLHVLRAHNAIASLRPRTFKDLHFLLEQLGHNRIQLGERTFEGLG 338  
QY 195 ALHVLEMSANPLDNGIPEGAFEGVTVFHIRIAEAK-----LTSVP-----KGLPPTLLEHL 247  
Db 339 QLEVLTLNDNQITE--VRVGAFSG--LFNVAVMNLSGNCLRSPLRVFQGL-DKLHSLHL 393  
QY 248 DYNKISTVELEDPKRYKELORGLGNKKTIDENGSLANIPRVREIHLNENKLLKIP--- 304  
Db 394 EHSGLCHVRLHTFAGLSGLRLFLRDNSSISIEQSLAGLSELELDLTTNRLTHLPRQL 453  
QY 305 -SGLPELKYLIQIFLHNSIARVGVNDFCPT-----VPMKKSLSYA----- 345  
Db 454 FQGLGHLEYL---LLSYNQLTLSAEVLGPLQRAFWLDISHNHLETLAEGFLSSIGRVRY 510  
QY 346 ISLFNPNPKYWMQPAFTER 364  
Db 511 LSLRNNSLQTFSPQGLER 529

## RESULT 34

US-08-473-089-50

; Sequence 50, Application US/08473089

; Patent No. 6342368

; GENERAL INFORMATION:

; APPLICANT: Mochly-Rosen, Daria

; APPLICANT: Ron, Dorit

; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

; TITLE OF INVENTION: Thereof

; NUMBER OF SEQUENCES: 265

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Morrison &amp; Foerster

; STREET: 2000 Pennsylvania Avenue, NW

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20006-1812

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/473,089

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: MURASHIGE, KATE H.

; REGISTRATION NUMBER: 29,959

; REFERENCE/DOCKET NUMBER: 2550-0025.22

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 887-1500

; TELEFAX: (202) 887-0763

; INFORMATION FOR SEQ ID NO: 50:

; SEQUENCE CHARACTERISTICS:

;  
; LENGTH: 603 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: Insulin-like growth factor bind.  
; INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33  
US-08-473-089-50

Query Match 13.7%; Score 272; DB 4; Length 603;  
Best Local Similarity 28.2%; Pred. No. 1.8e-18;  
Matches 90; Conservative 57; Mismatches 108; Indels 64; Gaps 12;

QY 102 DTRMLDQNNKIKKEIKENDFKGLTSLYGLILNNKLTTHPKAPLTKKLRRLYLSHNQL 161  
Db 219 ELRELDLSRNALRSVKANVFVHLPRLOKLYLDRNLITAVAPGAFGLMKALRWLDLSHNRV 278  
QY 162 SEI-----PLNL-----PKS-----LAELRIHENKVKKTKQKDTFGMN 194  
Db 279 AGLMEDTFPGLLGLHVLRAHNAIASLRPRTFKDLHFLLEQLGHNRIQLGERTFEGLG 338  
QY 195 ALHVLEMSANPLDNGIPEGAFEGVTVFHIRIAEAK-----LTSVP-----KGLPPTLLEHL 247  
Db 339 QLEVLTLNDNQITE--VRVGAFSG--LFNVAVMNLSGNCLRSPLRVFQGL-DKLHSLHL 393  
QY 248 DYNKISTVELEDPKRYKELORGLGNKKTIDENGSLANIPRVREIHLNENKLLKIP--- 304  
Db 394 EHSGLCHVRLHTFAGLSGLRLFLRDNSSISIEQSLAGLSELELDLTTNRLTHLPRQL 453  
QY 305 -SGLPELKYLIQIFLHNSIARVGVNDFCPT-----VPMKKSLSYA----- 345  
Db 454 FQGLGHLEYL---LLSYNQLTLSAEVLGPLQRAFWLDISHNHLETLAEGFLSSIGRVRY 510  
QY 346 ISLFNPNPKYWMQPAFTER 364  
Db 511 LSLRNNSLQTFSPQGLER 529

## RESULT 35

US-08-487-072A-50

; Sequence 50, Application US/08487072A

; Patent No. 6423684

; GENERAL INFORMATION:

; APPLICANT: Mochly-Rosen, Daria

; APPLICANT: Ron, Dorit

; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

; TITLE OF INVENTION: Thereof

; NUMBER OF SEQUENCES: 265

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Morrison &amp; Foerster

; STREET: 2000 Pennsylvania Avenue, NW

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20006-1812

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,072A

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: MURASHIGE, KATE H.

; REGISTRATION NUMBER: 29,959

; REFERENCE/DOCKET NUMBER: 2550-0025.20

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 887-1500

; TELEFAX: (202) 887-0763

INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 603 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Insulin-like growth factor bind.  
INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33  
US-08-487-072A-50

Query Match 13.7%; Score 272; DB 4; Length 603;

Best Local Similarity 28.2%; Pred. No. 1.8e-18;

Matches 90; Conservative 57; Mismatches 108; Indels 64; Gaps 12;

QY 102 DTRMLDQNNKKIKKIKENDFKGLTSLYGLILNNKLTQIHPKAFLLTKKLRRLYSHNQL 161  
DB 219 ELREDLSRNALRSVKANVFVHLPRLOKLYLDRNLITAVAGPAGFLGKALRWLDLSHNRY 278  
QY 162 SEI-----PLNL-----PKS-----LAEIRIHENKVKKIQDKTFKGMN 194  
DB 279 AGLMEDTFPGLLGLHLVLAHNAIASLRPTFKDLHLEELQLGHNRIRQLGERTTEGLG 338  
QY 195 ALHVEANSANPLDNGIEPGAFEGVTVFHRIAEAK-----LTSVP-----KGLPPTLLLEHL 247  
DB 339 QLEVLTLNDNOITE--VRVGAFCG--LFNVAVMNLSCNCLSLRPERVFQGL-DKLHSLHL 393  
QY 248 DYNKISVVELEDFRYKELQRLGNGNKITDIENGSLANIPRVREIHLNKKKKTP--- 304  
DB 394 EHCGLGHVRUHTFAGSLRLFLURDINSISIBEQSLAGLSLELEDLTTNRILTHLPQL 453  
QY 305 -SGLPKELQIILFIHNSIARVGVNDFCPT-----VPMKKKSLYSA----- 345  
DB 454 FQGLGHLEYL--LLSYNQLTISAEVLGPIQRAFWDLSHNHLETLAEGLFSSLRVRY 510  
QY 346 ISLFNNPVKVMQPATFR 364  
DB 511 LSLRNSLQTFSPQGLER 529

## RESULT 36

US-09-131-648-2  
Sequence 2, Application US/09131648  
Patent No. 6168920

GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.

APPLICANT: Yue, Henry

APPLICANT: Corley, Neil C.

APPLICANT: Guegler, Karl J.

APPLICANT: Patterson, Chandra

TITLE OF INVENTION: EXTRACELLULAR ADHESIVE PROTEINS

FILE REFERENCE: PF-0576 US

CURRENT APPLICATION NUMBER: US/09/131,648

CURRENT FILING DATE: 1998-08-10

NUMBER OF SEQ ID NOS: 5

SOFTWARE: PERL Program

SEQ ID NO 2

LENGTH: 708

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: -

OTHER INFORMATION: 2687731

US-09-131-648-2

## Query Match

Best Local Similarity 13.2%; Score 262; DB 4; Length 708;

Matches 95; Conservative 67; Mismatches 116; Indels 106; Gaps 18;

QY 74 CPFQCOYCSR-----VHCSDLGLTSVPTNIPDFTRMLDLQNNKKIKEIK-EN 119  
DB 29 CPRICTEIRPWFPTPSIYMEASTVDCNDLGLLTFFPARLPANTQILLQLTNNIAKIEYST 88

QY 120 DF-----KGLTSLYGLILNNKLTQIHPKAFLLTKKLRRLYLS 157  
DB 89 DFPVNLTLGLDSQNNLSSVTNINVKMPQLLSVYLEENKLTPEKCLSELNQLYIN 148  
QY 158 HNQLSEIP-----LNLPKSLAEIRIHENKVKKIQDKTFKGMNALHVEMSANPL-----DNN 209  
DB 149 HNLLSTISPGAFIGL-HNLLRLHLSNRLQMINSKWFDALPNLEITMIGENPIIRKDMN 207  
QY 210 GTEPGAFEGVTVFHRI--IAEAKITSVPGK-----LPPTLLLE-- 244  
DB 208 -FKP-----LINRLSVIAGINTEIPDNALVGLNLESLISFYDNRLIKRVPHVALQV 259  
QY 245 -----LHLDYNKISTVELEDFRYKELQRLGNG-NKITDIENGSLANIPRVREIHLN 298  
DB 260 VNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSLAVDNLPLDKTEATNN 319  
QY 299 -KLKKI-FSGLPKELQIILFIHNSIARVGVNDFCPTVPMKKKSLYSAISLFNNPVK-- 354  
DB 320 PRLSYIHPNAFFRDLPKFSLMNSNALSAL-YHGTIESLPNLKE-----ISHSNPIRCD 373  
QY 355 ---YWE-----MQPATFRCV 366  
DB 374 CVIRWMNKNKTNIRFEPDLSFCV 397

## RESULT 37

US-08-986-485-2

Sequence 2, Application US/08986485

Patent No. 6046030

GENERAL INFORMATION:

APPLICANT: WU, SHUJIAN

APPLICANT: SWEET, RAYMOND

APPLICANT: TRUNGH, ALEMSEGED

TITLE OF INVENTION: A HUMAN LIG-1 HOMOLOG (HLIG-1)

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESS: RATNER & PRESTIA

STREET: P.O. BOX 980

CITY: VALLEY FORGE

STATE: PA

COUNTRY: USA

ZIP: 19482

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/986,485

FILING DATE: 08-DEC-1997

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/059,448

FILING DATE: 22-SEP-1997

ATTORNEY/AGENT INFORMATION:

NAME: PRESTIA, PAUL F

REGISTRATION NUMBER: 23,031

REFERENCE/DOCKET NUMBER: GH-70264

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-407-0700

TELEFAX: 610-407-0701

TELEX: 846169

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1101 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-986-485-2

Query Match

13.0%; Score 259.5; DB 3; Length 1101;

Best Local Similarity 23.2%; Pred. No. 7.6e-17;  
Matches 83; Conservative 69; Mismatches 120; Indels 85; Gaps 10;

QY 78 CQCYRVVHCSDGLTSVPTNIPEDTRMLDQNNKIKETKENDFKGLTSLYGLIINNKKL 137  
Db 52 CTGAGSLDCCGGRLAALPCDLPSWTRSLNLSYNKLAELIDPAGFEDLNQEVYLNHEL 111  
QY 138 TKI-----HPKAFLT----- 147  
Db 112 TAVASLGGAGSQVVALFLOQQNRSLDGSQLKAYLSLEVLDLNNLNNITEVRNTYPPHGP 171  
QY 148 -----TKKLRLYLSHNSOLSEPL---NPKSLAELRIHENKV 182  
Db 172 IKELNLAGRNICITLGAFLDGLSLTLRLSKNRITQLPVRAFLPLR-LTOLDLNRKI 230  
QY 183 KTKOTKFGMNAHLVLEMSANPLDNNNGTEGAFEGVTVFHI-RIAAKLTSPKGL---- 238  
Db 231 RLIEGLTFQGLNSLEVLEKQNNISK--LTDGAFWGLSKMHVILHLEYDSLVEVNSGLYG 288  
QY 239 PPTLLEHLDYNKISTVELEDFKRYKELQRLGIGNKKITDIENGSLANIPTVREIHLNEN 298  
Db 289 LTALHQLHLSNNSIARHKGWFCQKHLHELVLFSFNNLRLDBESLAELSSLSVLRLSHN 348  
QY 299 KLKIPSG-LPELKYLIQILFHSNSTARVGVNDFCPTVPKMKKSLYSATLSFNNPVK 354  
Db 349 SISHIABGAPKGLRSURVLDLDRNEISGT-IEDTSCAFSGLEFG-HSKLTFLGNKIK 403

RESULT 38  
US-08-442-063A-33  
; Sequence 33, Application US/08442063A  
; Patent No. 5705609  
; GENERAL INFORMATION:  
; APPLICANT: RUOSLAHTI, ERKKI I.  
; APPLICANT: PIERSCHBACHER, MICHAEL D.  
; APPLICANT: CARDENAS, JOSE  
; APPLICANT: CRAIG, WILLIAM  
; APPLICANT: MULLEN, DANIEL G.  
; TITLE OF INVENTION: DECORIN FRAGMENTS AND METHODS OF  
; TITLE OF INVENTION: INHIBITING CELL REGULATORY FACTORS  
; NUMBER OF SEQUENCES: 62  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CAMPBELL AND FLORES  
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700  
; CITY: SAN DIEGO  
; STATE: CALIFORNIA  
; COUNTRY: UNITED STATES  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/442,063A  
; FILING DATE: 16-MAY-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/865,652  
; FILING DATE: 03-APR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CAMPBELL, CATHRYN A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LA 1454  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-535-9001  
; TELEFAX: 619-535-8949  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 96 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-442-063A-33

Query Match 12.9%; Score 256.5; DB 1; Length 96;  
Best Local Similarity 54.8%; Pred. No. 4.1e-18;  
Matches 51; Conservative 13; Mismatches 28; Indels 1; Gaps 1;  
QY 50 DEDNSLPTREPRSHFFPDLFPMCFGCQCYSRVHCSDGLTSVPTNIPEDTRMLDQ 109  
Db 3 DEASGIGP-EVPDDRDEPSPGVPFCPCQCHLRVVCSDGLDQKVPKDLPPDPTLLDQ 61  
QY 110 NKKIKEIKENDFKGLTSLYGLIINNKKLTTHP 142  
Db 62 NKKITEIKDGFKNLKNLHALILVNNKISKVSP 94

RESULT 39  
US-08-986-485-6  
; Sequence 6, Application US/08986485  
; Patent No. 6046030  
; GENERAL INFORMATION:  
; APPLICANT: WU, SHUIJIAN  
; APPLICANT: SWEET, RAYMOND  
; APPLICANT: TRUNEH, ALEMSEGED  
; TITLE OF INVENTION: A HUMAN LIG-1 HOMOLOG (HLIG-1)  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RATNER & PRESTIA  
; STREET: P.O. BOX 980  
; CITY: VALLEY FORGE  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19482  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/986,485  
; FILING DATE: 08-DEC-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/059,448  
; FILING DATE: 22-SEP-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PRESTIA, PAUL F  
; REGISTRATION NUMBER: 23,031  
; REFERENCE/DOCKET NUMBER: GH-70264  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-407-0700  
; TELEFAX: 610-407-0701  
; TELEX: 846169  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 353 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-986-485-6

Query Match 12.8%; Score 254; DB 3; Length 353;  
Best Local Similarity 28.1%; Pred. No. 5e-17;  
Matches 85; Conservative 52; Mismatches 133; Indels 32; Gaps 9;  
QY 72 PMCPCFGCQCY-----SRVVHCSDGLTSVPTNIPEDTRMLDQNNKIKETKENDFKGLT 125  
Db 4 PQCPVACTCSHDDYTDLSVFCSSKNLTPLPDDIPVTRALWLDGNNLSIPSAAFQNL 63  
QY 126 SLYGLIINNKKLTTHPFAFLTKKLRLYLSHNSOLSEIPLNL---PKSLAELRIHENKV 182  
Db 64 SLDFNLQGSWLRSLEPQALLQNLONLYLHLERNRLNLAVALGLTHTPSPSLSSNLL 123

[illegible]

```

Db 39 PACPAACVCSYDDADELSVFCSSRNLRTRLPDGVPGGTQALWLDGNNLSVPPAAAFQNL 98
QY 126 SLYGLILNNKLTTHPKAFLLTKKRLRLYLSHNQLSEIPLNL---PKSLAELRIHENKV 182
Db 99 SLGFLNLOGGQLSGLEPOALLGLENLCHLHLERNQLRSALGTFAITPALASGLSNNRL 158
QY 183 KKIQKDTFFKGMNALHVLMSANPLDNNGIEP-GAFEGVTVFHIRIAEAKLTSVPKGLPPT 241
Db 159 SRLEDGLFEGLSLWDLNLGNLSL---AVLPDAAFRGL-----GS 195
QY 242 LLEHLNDYKISTVELEDFKRYKELQRLGLGNKTIIDENGSLANIPRVREIHLNNK 301
Db 196 LRELVLNAGNRLAYLPALFSGLAELRELDLSNALRAIKANVFVQLPRLOKLYLDRNLIA 255
QY 302 KI-PSGLPELKYLIQIFLHNSIARVGVNDFCPTVPMKKSLYSALSIFNNPVKYWEMOP 360
Db 256 AVAPGAFLGLKALRWLDLSHNRVAGL-LEDTPFGLLGLR-----VLRSLHNAIA--SLRP 307
QY 361 ATFRCLVSRMSVOLGN 376
Db 308 RTFKDLHFLLEELQLGH 323

```

## RESULT 42

```

US-08-473-089-49
; Sequence 49, Application US/08473089
; Patent No. 6342368
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,089
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 605 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Insulin-like growth factor binding
; protein complex, Fig. 32
; INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-473-089-49

```

Query Match 12.3%; Score 246; DB 4; Length 605;  
 Best Local Similarity 25.3%; Pred. No. 6.8e-16;  
 Matches 80; Conservative 61; Mismatches 133; Indels 42; Gaps 9;

```

QY 72 PWCFFGCOCY-----SRVHCSDGLTSTVNTNIPDFTRMLDLQNNKIKEIKENDEKGLT 125
Db 39 PACPAACVCSYDDADELSVFCSSRNLRTRLPDGVPGGTQALWLDGNNLSVPPAAAFQNL 98
QY 126 SLYGLILNNKLTTHPKAFLLTKKRLRLYLSHNQLSEIPLNL---PKSLAELRIHENKV 182
Db 99 SLGFLNLOGGQLSGLEPOALLGLENLCHLHLERNQLRSALGTFAITPALASGLSNNRL 158
QY 183 KKIQKDTFFKGMNALHVLMSANPLDNNGIEP-GAFEGVTVFHIRIAEAKLTSVPKGLPPT 241
Db 159 SRLEDGLFEGLSLWDLNLGNLSL---AVLPDAAFRGL-----GS 195
QY 242 LLEHLNDYKISTVELEDFKRYKELQRLGLGNKTIIDENGSLANIPRVREIHLNNK 301
Db 196 LRELVLNAGNRLAYLPALFSGLAELRELDLSNALRAIKANVFVQLPRLOKLYLDRNLIA 255
QY 302 KI-PSGLPELKYLIQIFLHNSIARVGVNDFCPTVPMKKSLYSALSIFNNPVKYWEMOP 360
Db 256 AVAPGAFLGLKALRWLDLSHNRVAGL-LEDTPFGLLGLR-----VLRSLHNAIA--SLRP 307
QY 361 ATFRCLVSRMSVOLGN 376
Db 308 RTFKDLHFLLEELQLGH 323

```

## RESULT 43

```

US-08-487-072A-49
; Sequence 49, Application US/08487072A
; Patent No. 6423684
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,072A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 605 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Insulin-like growth factor binding
; protein complex, Fig. 32
; INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-487-072A-49

```

Query Match 12.3%; Score 246; DB 4; Length 605;



PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/059,448  
 FILING DATE: 22-SEP-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: PRESTIA, PAUL F  
 REGISTRATION NUMBER: 23,031  
 REFERENCE/DOCKET NUMBER: GH-70264  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 610-407-0700  
 TELEFAX: 610-407-0701  
 TELEX: 846169  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 180 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: LATRUT02  
 CLONE: 1352286  
 US-08-985-335-3

Query Match 12.0%; Score 239; DB 3; Length 180;  
 Best Local Similarity 25.6%; Pred. No. 5.6e-16;  
 Matches 58; Conservative 43; Mismatches 58; Indels 68; Gaps 3;

Qy 74 CPFCQCYRVHCSDGLTSVPTNIPFTRMLDLQNNKIKEIKENDPKGLTSLYLILN 133  
 Db 5 CPSCLCFRTVCMHLLLEAVPAVAP-QTSILDRLFRNIREIQPCAFRRRLNLTLLN 63  
 Qy 134 NNKLTHTPKAFLTTKKRLRLYLHSHNQLSEIPLNPKSLAELRIHENKVKIKQKDTFRGM 193  
 Db 64 NNQIKRIPSGAFEDLEMLKYL-----YKNEIOSIDRQAFKGL 102  
 Qy 194 NALHVLEMSANLQNNNGIEGAFEGVTVFHRIAEAKLTVPKGLPPTLLEHLHDYNKIS 253  
 Db 103 ASLE-----QYLHFNQTE 116  
 Qy 254 TVELEDPKRYKELQRLGIGNKKTIDTENGSLANIPRVREIHLNENKL 300  
 Db 117 TLDPSQHLPKLERLELHNRRITHLVPGTFNHLMSKRLRDSNTL 163

RESULT 47  
 US-08-985-335-3  
 Sequence 3, Application US/08985335  
 Patent No. 6080847  
 GENERAL INFORMATION:  
 APPLICANT: Hillman, Jennifer L.  
 APPLICANT: Yue, Henry  
 APPLICANT: Lal, Preeti  
 APPLICANT: Shah, Purvi  
 APPLICANT: Corley, Neil C.  
 TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
 TITLE OF INVENTION: PROLIFERATION  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Dr.  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/985,335  
 FILING DATE: Filed Herewith  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.  
 REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PF-0421 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-855-0555  
 TELEFAX: 650-845-4166  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 440 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: LATRUT02  
 CLONE: 1352286  
 US-08-985-335-3

Query Match 11.8%; Score 236; DB 3; Length 440;  
 Best Local Similarity 24.9%; Pred. No. 4.2e-15;  
 Matches 74; Conservative 52; Mismatches 117; Indels 54; Gaps 7;

Qy 78 CQCY-----RVHCSDGLTSVPTNIPFTRMLDLQNNKIKEIKENDPKGLTSLYLILN 133  
 Db 54 CDVYTYLHEKYLDCQERKLYVLPQWPQDLHMLLARNKIRTLKNMFKFKKLSLDLQ 113  
 Qy 134 NNKLTHTPKAFLTTKKRLRLYLHSHNQLSEIPLNPKSLAELRIHEN----- 180  
 Db 114 ONELSKIESAFGLKNTLLLOHNOIKVLTVEEVIYTP-LLSYRLYDNPWHCTCEIE 172  
 Qy 181 -----KVKIKQKDTFRGMNALHVLEMSANLQNNNGIEP----- 213  
 Db 173 TLISMLQIPNRNLGNVAKCESPOEQKNKKLQIKSEQLCNEEQQLDPKQVSGRPVI 232  
 Qy 214 -----GAFEGVTVFHRIAEAK---LTSVPKGLPPTLLEHLHDYNKISTVELEDEKRYKE 265  
 Db 233 KPEVDSTFCHYVFPITQTLDCRKRKLKVPNNIPDPDIVKLDLSYNKINOLRPKEFEDVHE 292  
 Qy 266 LORGLGNKKTIDTENGSLANIPRVREIHLNENKLLKIPSG-LPELKYLIQIIFLHNS 321  
 Db 293 LKKLNLSSNGIEFIDPAFLGLTHLEELDLSNNSLQNFQVLELDLYFLKLLWLRDN 349

RESULT 48  
 US-09-410-372-3  
 Sequence 3, Application US/09410372  
 Patent No. 6281334  
 GENERAL INFORMATION:  
 APPLICANT: Hillman, Jennifer L.  
 APPLICANT: Yue, Henry  
 APPLICANT: Lal, Preeti  
 APPLICANT: Shah, Purvi  
 APPLICANT: Corley, Neil C.  
 TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
 TITLE OF INVENTION: PROLIFERATION  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Dr.  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/410,372  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/985,335  
 FILING DATE:

ATTORNEY/AGENT INFORMATION:  
 NAME: Billings, Lucy J.  
 REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PF-0421 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-855-0555  
 TELEFAX: 650-845-4166  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 440 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: LATRUT02  
 CLONE: 1352286  
 US-09-410-372-3

Query Match 11.8%; Score 236; DB 4; Length 440;  
 Best Local Similarity 24.9%; Pred. No. 4.2e-15;  
 Matches 74; Conservative 52; Mismatches 117; Indels 54; Gaps 7;  
 QY 78 CQCY----RVHCSDLGTSVPTNIPDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133  
 Db 54 CQVYTLHEKYLDCQERKLYVLPQWQDLHLMLARKNKIRTLKNNMFSKFKLKSLDLQ 113  
 QY 134 NKKLTIKHPKAFITTKKRLRYLSHNQL-----SEIPLNPKSLAELRIHEN----- 180  
 Db 114 QNEISKIESEAFGLKLTLLQHQIKVLTEEVFVTP-LLSVRLYDNPWCHTCIE 172  
 QY 181 -----KVKIKQDTEKGMNALHVLMSANPLDNGIEP----- 213  
 Db 173 TLISMLQIPRNLGNVAKCESPQKNNKLRQKSEQLCNEEKEQLDKPQVSGRPPI 232  
 QY 214 -----GAFEGVTVFHRIAEAK---LTSVPKGLPPTLELHLDYNNKISTVELEDFKRYKE 265  
 Db 233 KPEVDSTFCHNVFPQTLDCKRKELKVPNNIPDIVKLDLSYNNKINQLRPFEDVHE 292  
 QY 266 LQRLGIGNNKITDIENGSLANIPRVREIHLNENKLIKIPSG-LPELYLOIIFLHSN 321  
 Db 293 LAKNLSSNGIEFIDPAFLGLTHLEELDLSSNLSQNFYGVLEDLYFLKLLWRDN 349

RESULT 49  
 PCT-US91-09055-4  
 Sequence 4, Application PC/TUS9109055  
 GENERAL INFORMATION:  
 APPLICANT: Rothberg, Jonathan Marc and Artavanis-Tsakonas, Spyridon  
 TITLE OF INVENTION: Purified SLIT protein and Sequence Elements Thereof  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Yale University  
 ADDRESSEE: Office of Cooperative Research  
 STREET: 246 Church Street  
 CITY: Suite 401  
 CITY: New Haven  
 STATE: Connecticut  
 COUNTRY: USA  
 ZIP: 06510  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage  
 COMPUTER: Apple Macintosh  
 OPERATING SYSTEM: Macintosh 6.0.5  
 SOFTWARE: Microsoft Word 4.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US91/09055  
 FILING DATE: 19911127  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/07/624,135  
 FILING DATE: 7-DEC-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Barth, Richard J.

REGISTRATION NUMBER: 28,180  
 REFERENCE/DOCKET NUMBER: 900964/RSB  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 972-1400  
 TELEFAX: (212) 370-1622  
 TELEFAX: 236268  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 224 amino acids  
 TYPE: AMINO ACIDS  
 TOPOLOGY: Linear  
 MOLECULE TYPE: protein  
 FEATURE:  
 NAME/KEY: Flank-LRR-Flank 2  
 LOCATION: 1 to 224  
 IDENTIFICATION METHOD: similarity to other Flank-LRR-  
 OTHER INFORMATION: mediates adhesive events  
 PCT-US91-09055-4

Query Match 11.1%; Score 222; DB 5; Length 224;  
 Best Local Similarity 22.3%; Pred. No. 3.8e-14;  
 Matches 69; Conservative 49; Mismatches 89; Indels 102; Gaps 8;  
 QY 74 CPFGCCYSRVHCSDLGTSVPTNIPDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133  
 Db 1 CPHPCCADGIVDCREKSLTSVPVTLDPDITDVRLEQNF----- 40  
 QY 134 NKKLTIKHPKAFITTKKRLRYLSHNQLSEI---PLNPKSLAELRIHENKVKIKQDTE 190  
 Db 41 -----TELPKPSFSPFRLRRIDLSNNISRTAHDAISGLQTLTVLYGNKIKDLPSTGV 96  
 QY 191 KGMNALHVLMSANPLDNGIEPQAFEGTVFVHRIAEAKLTSVPKGLPPTLELHLDYN 250  
 Db 97 KUGSLRLLLN-----N 110  
 QY 251 KISTVELEDFKRYKELQRLGIGNNKITDIENGSLANIPRVREIHLNENKLIKIPSGLP-- 308  
 Db 111 EITCIRKDAFRDLHSLSLLSLYDNNISQISLANGTDFDAMKSMKTVHLAKN-----PFI 161  
 QY 309 ---ELKYLIQIIFLHSNLSIARVGVNDFCTVPKMKKSLYSALSIFNNPVKYMOPATFRC 365  
 Db 162 CDCNLRL-ADYLHKNPIETSGAR--CESPKRMHRR-----RIESLREEKFKC 206  
 QY 366 VLRSMSVOL 374  
 Db 207 SWGELRMKL 215

RESULT 50  
 US-09-232-160-17  
 Sequence 17, Application US/09232160  
 Patent No. 6368794  
 GENERAL INFORMATION:  
 APPLICANT: Steve Daniel  
 APPLICANT: James Gilmore  
 APPLICANT: Susan G. Stuart  
 APPLICANT: Laura Stuve  
 TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL  
 TITLE OF INVENTION: PROLIFERATION  
 FILE REFERENCE: PA-0003 US  
 CURRENT APPLICATION NUMBER: US/09/232,160  
 CURRENT FILING DATE: 1999-01-15  
 NUMBER OF SEQ ID NOS: 23  
 SOFTWARE: PERL Program  
 SEQ ID NO 17  
 LENGTH: 298  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 OTHER INFORMATION: 159452  
 US-09-232-160-17

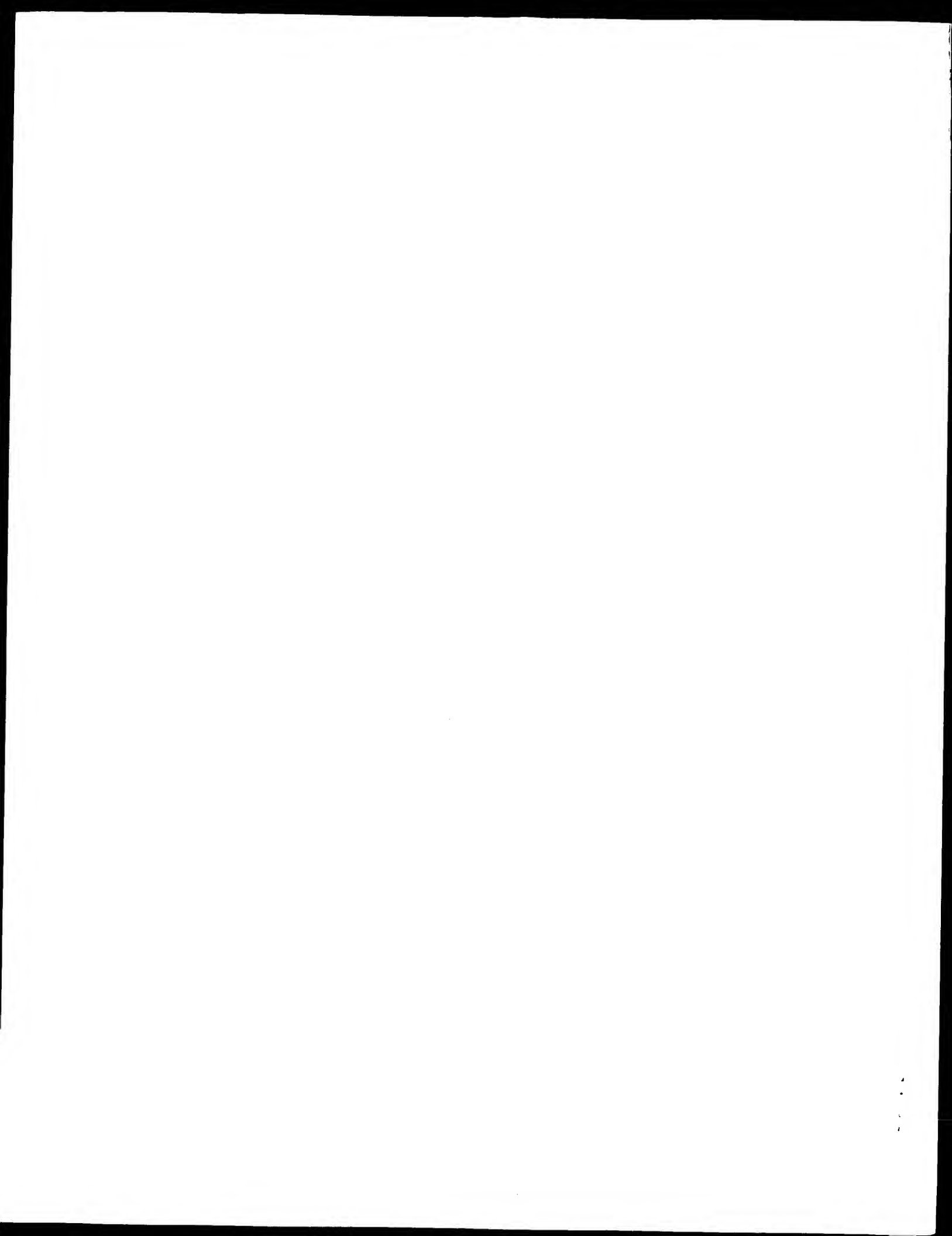
Query Match 10.7%; Score 212.5; DB 4; Length 298;



Best Local Similarity 27.5%; Pred. No. 5e-13;  
Matches 74; Conservative 41; Mismatches 101; Indels 53; Gaps 10;

QY 51 EDNSLFTPREPSHFFPPDLEFPMCPFGCQCYSRVHCHSDGLTSTVPTNIPFDTRMLDLON 110  
Db : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : :  
75 KDEAITPLPPKKEN---DEMPCTCL-CVCLSGSVYCEEVDIDAVPP-LPKESAYLYARF 128  
QY 111 NKIKIKENDFKGLTSLYLILNNKLTKHPKAFLTTKKLRRLYLSHNOLSEIPLNLPK 170  
Db : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : :  
129 NKIKLTKAKDFADIPNLRDFTGNLIEDGTFSKLSLEELSLSAENQLLKLVP-LPP 187  
QY 171 SLAELRIHENKVKK--IQKDTFKGMNALHVLMSANPLDNNNGIEPGAEGVTVFHIRIAE 228  
Db : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : :  
188 KLTFLNAKYNKTKSRGIKANAFKLNLTFLY-----LDHNALE----- 226  
QY 229 AKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNKKITDIENGLANIP 288  
Db : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : :  
227 ----SVPLNLPESLRVHLOFNFIASITDDTFCKAND-----TSYIRD----- 265  
QY 289 RVREIHLNKK--LKKIPSGLPKYLQI 315  
Db : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : :  
266 RIEEIRLEGNPIVLGKHPNSFICLRLPI 294

Search completed: January 24, 2003, 12:27:03  
Job time : 24 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 24, 2003, 12:26:46 ; Search time 12 Seconds  
(without alignments)

637.306 Million cell updates/sec

Title: US-09-944-457-2

Perfect score: 1992

Sequence: 1 MKEYVLLFLALCSAKPFS.....PATFRCLVSRMSVQLNGFM 379

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 50 summaries

Database : Published\_Applications\_AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*

2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*

3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*

4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*

5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*

6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*

7: /cgn2\_6/ptodata/2/pubpaa/FCRUS\_PUBCOMB.pep.\*

8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*

9: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*

10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*

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12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*

13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1992	100.0	379	9	US-09-944-413-2
2	1992	100.0	379	9	US-09-944-413-2
3	1992	100.0	379	9	US-09-944-896-2
4	1992	100.0	379	9	US-09-944-944-2
5	1992	100.0	379	9	US-09-944-907-2
6	1992	100.0	379	9	US-09-944-929-2
7	1992	100.0	379	9	US-10-028-072-328
8	1992	100.0	379	10	US-09-866-028-2
9	1992	100.0	379	10	US-09-944-449-2
10	1992	100.0	379	10	US-09-944-457-2
11	1992	100.0	379	10	US-09-944-862-2
12	1992	100.0	379	10	US-09-945-587-2
13	1992	100.0	379	10	US-09-945-015-2
14	1992	100.0	379	10	US-09-944-396-2
15	1992	100.0	379	10	US-09-944-097-2
16	1992	100.0	379	10	US-09-944-432-2
17	1992	100.0	379	10	US-09-943-762-2
18	1992	100.0	379	10	US-09-944-654-2
19	1992	100.0	379	10	US-09-943-851A-2

20	406.5	20.4	155	10	US-09-925-301-1561	Sequence 1561, Ap
21	393	19.7	353	10	US-09-925-301-980	Sequence 980, App
22	366	18.4	421	9	US-10-028-072-302	Sequence 302, App
23	363.5	18.2	674	9	US-10-028-072-36	Sequence 36, Appl
24	331.5	16.6	623	10	US-09-764-870-276	Sequence 276, App
25	331.5	16.6	649	9	US-10-063-547-132	Sequence 132, App
26	331.5	16.6	649	9	US-10-004-551-6	Sequence 6, Appli
27	331.5	16.6	649	9	US-10-174-590-384	Sequence 384, App
28	331.5	16.6	649	9	US-10-176-758-384	Sequence 384, App
29	331.5	16.6	649	9	US-10-063-616-132	Sequence 132, App
30	331.5	16.6	649	9	US-10-175-737-384	Sequence 384, App
31	331.5	16.6	649	12	US-10-006-867-132	Sequence 132, App
32	331.5	16.6	649	12	US-10-052-586-384	Sequence 384, App
33	329	16.5	642	9	US-10-028-072-370	Sequence 370, App
34	323	16.2	415	10	US-09-925-301-1192	Sequence 1192, Ap
35	313.5	15.7	660	9	US-09-905-291A-28	Sequence 28, Appl
36	313.5	15.7	660	9	US-10-066-500-115	Sequence 115, App
37	313.5	15.7	660	9	US-09-902-853-28	Sequence 28, Appl
38	313.5	15.7	660	9	US-09-907-824-28	Sequence 28, Appl
39	313.5	15.7	660	9	US-09-907-841-28	Sequence 28, Appl
40	313.5	15.7	660	9	US-09-904-011-28	Sequence 28, Appl
41	313.5	15.7	660	9	US-10-028-072-350	Sequence 350, App
42	313.5	15.7	660	10	US-09-909-320-28	Sequence 28, Appl
43	313.5	15.7	660	10	US-09-909-088B-28	Sequence 28, Appl
44	313	15.7	1480	12	US-10-011-064-5	Sequence 5, Appli
45	309	15.5	1523	9	US-10-174-590-290	Sequence 290, App
46	309	15.5	1523	9	US-10-176-758-290	Sequence 290, App
47	309	15.5	1523	9	US-10-175-737-290	Sequence 290, App
48	309	15.5	1523	12	US-10-011-064-2	Sequence 2, Appli
49	309	15.5	1523	12	US-10-052-586-290	Sequence 290, App
50	304.5	15.3	513	9	US-10-063-547-124	Sequence 124, App

ALIGNMENTS

RESULT 1

US-09-944-413-2

; Sequence 2, Application US/09944413

; Patent No. US2002015600A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Botstein, David

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Hillan, Kenneth

; APPLICANT: Kljavin, Ivar

; APPLICANT: Napier, Mary

; APPLICANT: Roy, Margaret

; APPLICANT: Tumas, Daniel

; APPLICANT: Wood, William

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P2548P1C1

; CURRENT APPLICATION NUMBER: US/09/944,413

; PRIOR FILING DATE: 2001-09-26

; PRIOR APPLICATION NUMBER: 09/866,028

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/067,411

; PRIOR FILING DATE: December 3, 1997

; PRIOR APPLICATION NUMBER: 60/069,334

; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069,335

; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069,278

; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069,425

Query Match 100.0%; Score 1992; DB 9; Length 379;



	Query Match	100.0%; Score 1992; DB 9;	Length 379;
	Best Local Similarity	100.0%; Pred. No. 2e-159;	
	Matches 379; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MKEYVLLFLALCSAKFFSPESHIALKNMMLKOWEDTDDDDDDDDDDDEDSLSFPTRE	60	
dDb			
	1 MKEYVLLFLALCSAKFFSPSHIALKNMMLKOWEDTDDDDDDDDDDDEDSLSFPTRE	60	
QY	61 PRSHEFFPDLPFMGFCQCYSRWVHCSDLGLTSVTPNPFOTRMLDLONNKIKEIKND	120	
db	61 PRSHEFFPDLPFMGFCQCYSRWVHCSDLGLTSVTPNPFOTRMLDLONNKIKEIKND	120	

	Query Match	100.0%;	Score 1992;	DB 9;	Length 379;	
	Best Local Similarity	100.0%;	Pred. No. 2e-159;			
	Matches 379;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
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Dd	1	MKEVYLLFLALCSAKFFFSF	SHTALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDDDDSLFPTR	60		
Qy	61	PRSHFFPDLFPMCFCGQCYSRVVHCSDGLGTSVPTNIPEDTRMLDQNKNIKEIKEND	120			
Dd	61	PRSHFFPDLFPMCFCGQCYSRVVHCSDGLGTSVPTNIPEDTRMLDQNKNIKEIKEND	120			
Qy	121	FKGUTSLYGLILNNNKLTUKIHPKAFLTKKLRLRYLSHNQLSEIPLNPKSLAEURLHEN	180			
Dd	121	FKGUTSLYGLILNNNKLTUKIHPKAFLTKKLRLRYLSHNQLSEIPLNPKSLAEURLHEN	180			
Qy	181	KVKTIQKDTFKGMNALHVLEMSANPLDNNGTEPGAFEGVTVFHRIAEAKLTSVPKGLPP	240			
Dd	181	KVKTIQKDTFKGMNALHVLEMSANPLDNNGTEPGAFEGVTVFHRIAEAKLTSVPKGLPP	240			

QY 241 TLELHLDYKNIKSTVELEDFKRYKELQRLGLGNKNTIDENGSLANIPRVREIHLNENKL 300  
 Db 241 TLELHLDYKNIKSTVELEDFKRYKELQRLGLGNKNTIDENGSLANIPRVREIHLNENKL 300  
 QY 301 KKIPSGLPKLYLQIIFLHNSNSTARVGVNDFCPTVPKMKKSLYSALSIFLNNPVKYWEMQ 360  
 Db 301 KKIPSGLPKLYLQIIFLHNSNSTARVGVNDFCPTVPKMKKSLYSALSIFLNNPVKYWEMQ 360  
 QY 361 ATRCVLSRMSVOLGNFGM 379  
 Db 361 ATRCVLSRMSVOLGNFGM 379  
 RESULT 6  
 US-09-944-929-2  
 ; Sequence 2, Application US/09944929  
 ; Publication No. US20020197612A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gerritsen, Mary  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul  
 ; APPLICANT: Grimaldi, Christopher  
 ; APPLICANT: Gurney, Austin  
 ; APPLICANT: Hillan, Kenneth  
 ; APPLICANT: Kljavin, Ivar  
 ; APPLICANT: Napier, Mary  
 ; APPLICANT: Roy, Margaret  
 ; APPLICANT: Tomas, Daniel  
 ; APPLICANT: Wood, William  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P2548P1C1  
 ; CURRENT APPLICATION NUMBER: US/09/944, 929  
 ; PRIOR FILING DATE: 2001-08-31  
 ; PRIOR APPLICATION NUMBER: 09/866, 028  
 ; PRIOR FILING DATE: 2001-05-25  
 ; NUMBER OF SEQ ID NOS: 120  
 ; SEQ ID NO 2  
 ; LENGTH: 379  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-09-944-929-2  
 Query Match 100.0%; Score 1992; DB 9; Length 379;  
 Best Local Similarity 100.0%; Pred. No. 2e-159;  
 Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 1 MKEYVLLFLALCSAKPFFSPSHIALKNMMLKMDTDDDDDDDDDDDDDDDDDDDDDDNSLFPPTRE 60  
 QY 61 PRSHFFPDLFPMCPFCQCYSRVHCHSDGLTSVPTNPDPFRMLDLQNNKIKELKEND 120  
 Db 61 PRSHFFPDLFPMCPFCQCYSRVHCHSDGLTSVPTNPDPFRMLDLQNNKIKELKEND 120  
 QY 121 FKGLTSLYGLLNNKLTIKHPKAFLTTRKKRLRLYLHNSQLSEIPLNLPKSLAELRIHEN 180  
 Db 121 FKGLTSLYGLLNNKLTIKHPKAFLTTRKKRLRLYLHNSQLSEIPLNLPKSLAELRIHEN 180  
 QY 181 KVKIKQDFTKGMNALHVLMSANPLDNGIEPGAFEGVTVFHRIAEAKLTSVPKGLPP 240  
 Db 181 KVKIKQDFTKGMNALHVLMSANPLDNGIEPGAFEGVTVFHRIAEAKLTSVPKGLPP 240  
 QY 241 TLELHLDYKNIKSTVELEDFKRYKELQRLGLGNKNTIDENGSLANIPRVREIHLNENKL 300  
 Db 241 TLELHLDYKNIKSTVELEDFKRYKELQRLGLGNKNTIDENGSLANIPRVREIHLNENKL 300  
 QY 301 KKIPSGLPKLYLQIIFLHNSNSTARVGVNDFCPTVPKMKKSLYSALSIFLNNPVKYWEMQ 360

Db 301 KKIPSGLPKLYLQIIFLHNSNSTARVGVNDFCPTVPKMKKSLYSALSIFLNNPVKYWEMQ 360  
 QY 361 ATRCVLSRMSVOLGNFGM 379  
 Db 361 ATRCVLSRMSVOLGNFGM 379  
 RESULT 7  
 US-10-028-072-328  
 ; Sequence 328, Application US/10028072  
 ; Publication No. US20030004311A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Beresini, Maureen  
 ; APPLICANT: Deforge, Laura  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Sherwood, Steven  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tomas, Daniel  
 ; APPLICANT: Watanabe, Colin K  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Zhang  
 ; TITLE OF INVENTION:  
 ; FILE REFERENCE:  
 ; CURRENT APPLICATION NUMBER: US/10/028, 072  
 ; CURRENT FILING DATE: 2001-12-19  
 ; PRIOR APPLICATION NUMBER: 60/049911  
 ; PRIOR FILING DATE: 1997-06-18  
 ; PRIOR APPLICATION NUMBER: 60/056974  
 ; PRIOR FILING DATE: 1997-08-26  
 ; PRIOR APPLICATION NUMBER: 60/059113  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/059115  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/059117  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/059122  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/059184  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/059263  
 ; PRIOR FILING DATE: 1997-09-18  
 ; PRIOR APPLICATION NUMBER: 60/059352  
 ; PRIOR FILING DATE: 1997-09-19  
 ; PRIOR APPLICATION NUMBER: 60/059588  
 ; PRIOR FILING DATE: 1997-09-19  
 ; PRIOR APPLICATION NUMBER: 60/059836  
 ; PRIOR FILING DATE: 1997-09-24  
 ; PRIOR APPLICATION NUMBER: 60/062250  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/062285  
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 ; PRIOR FILING DATE: 1997-10-24  
 ; PRIOR APPLICATION NUMBER: 60/063045  
 ; PRIOR FILING DATE: 1997-10-24  
 ; PRIOR APPLICATION NUMBER: 60/063082  
 ; PRIOR FILING DATE: 1997-10-31  
 ; PRIOR APPLICATION NUMBER: 60/063127  
 ; PRIOR FILING DATE: 1997-10-24  
 ; PRIOR APPLICATION NUMBER: 60/063327



1	PRIOR APPLICATION NUMBER: 60/083322
2	PRIOR FILING DATE: 1998-04-28
3	PRIOR APPLICATION NUMBER: 60/083545
4	PRIOR FILING DATE: 1998-04-29
5	PRIOR APPLICATION NUMBER: 60/084600
6	PRIOR FILING DATE: 1998-05-07
7	PRIOR APPLICATION NUMBER: 60/084627
8	PRIOR FILING DATE: 1998-05-07
9	PRIOR APPLICATION NUMBER: 60/084637
10	PRIOR FILING DATE: 1998-05-07
11	PRIOR APPLICATION NUMBER: 60/085149
12	PRIOR FILING DATE: 1998-05-12
13	PRIOR APPLICATION NUMBER: 60/085323
14	PRIOR FILING DATE: 1998-05-13
15	PRIOR APPLICATION NUMBER: 60/085338
16	PRIOR FILING DATE: 1998-05-13
17	PRIOR APPLICATION NUMBER: 60/085339
18	PRIOR FILING DATE: 1998-05-13
19	PRIOR APPLICATION NUMBER: 60/085579
20	PRIOR FILING DATE: 1998-05-15
21	PRIOR APPLICATION NUMBER: 60/085697
22	PRIOR FILING DATE: 1998-05-15
23	PRIOR APPLICATION NUMBER: 60/085704
24	PRIOR FILING DATE: 1998-05-15
25	PRIOR APPLICATION NUMBER: 60/086414
26	PRIOR FILING DATE: 1998-05-22
27	PRIOR APPLICATION NUMBER: 60/086430
28	PRIOR FILING DATE: 1998-05-22
29	PRIOR APPLICATION NUMBER: 60/087106
30	PRIOR FILING DATE: 1998-05-28
31	PRIOR APPLICATION NUMBER: 60/088026
32	PRIOR FILING DATE: 1998-06-04
33	PRIOR APPLICATION NUMBER: 60/088730
34	PRIOR FILING DATE: 1998-06-10
35	PRIOR APPLICATION NUMBER: 60/088741
36	PRIOR FILING DATE: 1998-06-10
37	PRIOR APPLICATION NUMBER: 60/088810
38	PRIOR FILING DATE: 1998-06-10
39	PRIOR APPLICATION NUMBER: 60/088858
40	PRIOR FILING DATE: 19/98-06-11
41	PRIOR APPLICATION NUMBER: 60/089532
42	PRIOR FILING DATE: 1998-06-17
43	PRIOR APPLICATION NUMBER: 60/089599
44	PRIOR FILING DATE: 1998-06-17
45	PRIOR APPLICATION NUMBER: 60/089907
46	PRIOR FILING DATE: 1998-06-18
47	PRIOR APPLICATION NUMBER: 60/089947
48	PRIOR FILING DATE: 1998-06-19
49	PRIOR APPLICATION NUMBER: 60/090349
50	PRIOR FILING DATE: 1998-06-23
51	PRIOR APPLICATION NUMBER: 60/090429
52	PRIOR FILING DATE: 1998-06-24
53	PRIOR APPLICATION NUMBER: 60/090445
54	PRIOR FILING DATE: 1998-06-24
55	PRIOR APPLICATION NUMBER: 60/090538
56	PRIOR FILING DATE: 1998-06-24
57	PRIOR APPLICATION NUMBER: 60/090863
58	PRIOR FILING DATE: 1998-06-26
59	PRIOR APPLICATION NUMBER: 60/091360
60	PRIOR FILING DATE: 1998-07-01
61	PRIOR APPLICATION NUMBER: 60/091519
62	PRIOR FILING DATE: 1998-07-02
63	PRIOR APPLICATION NUMBER: 60/091982
64	PRIOR FILING DATE: 1998-07-07

Best Local Similarity: 100.0%; Pred. NO: 2E-139;  
Matches 379: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MKEYVLLFLALCSAKPFFSHTALKNNMLKDMEDTDDDDDDDDDDDEDNSLFPTRR       
Db	.1	MKEYVLLFLALCSAKPFFSHTALKNNMLKDMEDTDDDDDDDDDDDEDNSLFPTRR       

QY 61 PRSHFFPDLPMPGCGOCYSRVVHCSDLGLTSVPTNIPDTRMLDQNNKIKEIKEND 120  
Db 61 PRSHFFPDLPMPGCGOCYSRVVHCSDLGLTSVPTNIPDTRMLDQNNKIKEIKEND 120  
QY 121 FKGLTSLYGLILNNKLTTHPKAFLLTKKRLRLYLSHNSLSEIPLNPKSLAEHLRIHEN 180  
Db 121 FKGLTSLYGLILNNKLTTHPKAFLLTKKRLRLYLSHNSLSEIPLNPKSLAEHLRIHEN 180  
QY 181 KVKIKQDFTFGMNAHVLMSANPLDNNGIEPGAEGVTVFHRIAEAKLTSPKGLPP 240  
Db 181 KVKIKQDFTFGMNAHVLMSANPLDNNGIEPGAEGVTVFHRIAEAKLTSPKGLPP 240  
QY 241 TLELHLDYNNKISTVELEDFKRYKELQRLGLGNKKTIDENGSLANIIPRVREIHLNENKL 300  
Db 241 TLELHLDYNNKISTVELEDFKRYKELQRLGLGNKKTIDENGSLANIIPRVREIHLNENKL 300  
QY 301 KPIPGLPELKYLIQIFLHNSIARVGVNDFCPTVPKMKKSLYSALSIFNPNVYEMOP 360  
Db 301 KPIPGLPELKYLIQIFLHNSIARVGVNDFCPTVPKMKKSLYSALSIFNPNVYEMOP 360  
QY 361 ATFRVLSRMSVOLGNFGM 379  
Db 361 ATFRVLSRMSVOLGNFGM 379

## RESULT 8

US-09-866-028-2  
; Sequence 2, Application US/09866028  
; Patent No. US2002058309A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/866,028  
; CURRENT FILING DATE: 2001-05-25  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 2  
; LENGTH: 379  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-866-028-2

Query Match 100.0%; Score 1992; DB 10; Length 379;  
Best Local Similarity 100.0%; Pred. No. 2e-159;  
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKEYVLLFLALCSAKFFSFHIALKNMMLKMDMTDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD 60  
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QY 61 PRSHFFPDLPMPGCGOCYSRVVHCSDLGLTSVPTNIPDTRMLDQNNKIKEIKEND 120  
Db 61 PRSHFFPDLPMPGCGOCYSRVVHCSDLGLTSVPTNIPDTRMLDQNNKIKEIKEND 120  
QY 121 FKGLTSLYGLILNNKLTTHPKAFLLTKKRLRLYLSHNSLSEIPLNPKSLAEHLRIHEN 180

Db 121 FKGLTSLYGLILNNKLTTHPKAFLLTKKRLRLYLSHNSLSEIPLNPKSLAEHLRIHEN 180  
QY 181 KVKIKQDFTFGMNAHVLMSANPLDNNGIEPGAEGVTVFHRIAEAKLTSPKGLPP 240  
Db 181 KVKIKQDFTFGMNAHVLMSANPLDNNGIEPGAEGVTVFHRIAEAKLTSPKGLPP 240  
QY 241 TLELHLDYNNKISTVELEDFKRYKELQRLGLGNKKTIDENGSLANIIPRVREIHLNENKL 300  
Db 241 TLELHLDYNNKISTVELEDFKRYKELQRLGLGNKKTIDENGSLANIIPRVREIHLNENKL 300  
QY 301 KPIPGLPELKYLIQIFLHNSIARVGVNDFCPTVPKMKKSLYSALSIFNPNVYEMOP 360  
Db 301 KPIPGLPELKYLIQIFLHNSIARVGVNDFCPTVPKMKKSLYSALSIFNPNVYEMOP 360  
QY 361 ATFRVLSRMSVOLGNFGM 379  
Db 361 ATFRVLSRMSVOLGNFGM 379

## RESULT 9

US-09-944-449-2  
; Sequence 2, Application US/09944449  
; Patent No. US20020102647A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/944,449  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/866,028  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/067,411  
; PRIOR FILING DATE: December 3, 1997  
; PRIOR APPLICATION NUMBER: 60/069,334  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,335  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,278  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,425  
; PRIOR FILING DATE: December 12, 1997  
; PRIOR APPLICATION NUMBER: 60/069,696  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,694  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,702  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,870  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/069,873  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/068,017  
; PRIOR FILING DATE: December 18, 1997  
; PRIOR APPLICATION NUMBER: 60/070,440  
; PRIOR FILING DATE: January 5, 1998  
; PRIOR APPLICATION NUMBER: 60/074,086  
; PRIOR FILING DATE: February 9, 1998

[illegible]

; PRIOR APPLICATION NUMBER: 60/112,850  
 ; PRIOR FILING DATE: December 16, 1998  
 ; PRIOR APPLICATION NUMBER: 60/113,296  
 ; PRIOR FILING DATE: December 22, 1998  
 ; PRIOR APPLICATION NUMBER: 60/146,222  
 ; PRIOR FILING DATE: July 28, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US98/19330  
 ; PRIOR FILING DATE: September 16, 1998  
 ; PRIOR APPLICATION NUMBER: PCT/US98/25108  
 ; PRIOR FILING DATE: December 1, 1998  
 ; PRIOR APPLICATION NUMBER: 09/216,021  
 ; PRIOR FILING DATE: December 16, 1998  
 ; PRIOR APPLICATION NUMBER: 09/218,517  
 ; PRIOR FILING DATE: December 22, 1998  
 ; PRIOR APPLICATION NUMBER: 09/254,311  
 ; PRIOR FILING DATE: March 3, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/12252  
 ; PRIOR FILING DATE: June 22, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090  
 ; PRIOR FILING DATE: September 15, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28409  
 ; PRIOR FILING DATE: No. US20020110859A1ember 30, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313  
 ; PRIOR FILING DATE: No. US20020110859A1ember 30, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28301  
 ; PRIOR FILING DATE: December 1, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095  
 ; PRIOR FILING DATE: December 16, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US00/03565  
 ; PRIOR FILING DATE: February 11, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414  
 ; PRIOR FILING DATE: February 22, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/05841  
 ; PRIOR FILING DATE: March 2, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/08439  
 ; PRIOR FILING DATE: March 30, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/14042  
 ; PRIOR FILING DATE: May 22, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/20710  
 ; PRIOR FILING DATE: July 28, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/32678  
 ; PRIOR FILING DATE: December 1, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US01/06520  
 ; PRIOR FILING DATE: February 28, 2001  
 ; NUMBER OF SEQ ID NOS: 120  
 ; SEQ ID NO 2  
 ; LENGTH: 379  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-09-944-457-2  
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 Best Local Similarity 100.0%; Pred. No. 2e-159;  
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 QY 1 MKEYVLLFLALCSAKPFTSPSHIAKNNMLKDMEDTDDDDDDDDDDDDNSLPPTRE 60  
 DB 1 MKEYVLLFLALCSAKPFTSPSHIAKNNMLKDMEDTDDDDDDDDDDDDNSLPPTRE 60  
 QY 61 PRSHFPFDLPFCPPCCQCYSRVHCSDLGLTSVPTNIPFDTRMLDQNNKIKEKEND 120  
 DB 61 PRSHFPFDLPFCPPCCQCYSRVHCSDLGLTSVPTNIPFDTRMLDQNNKIKEKEND 120  
 QY 121 FGLTSLYGLILNNKLTWKHPKAFLLTKKRLRLYLSHNLSEIPLNPKSLAEIRIHEN 180  
 DB 121 FGLTSLYGLILNNKLTWKHPKAFLLTKKRLRLYLSHNLSEIPLNPKSLAEIRIHEN 180  
 QY 181 KVKIKQDFTKGMNALHVLMSANPLDNNNGIEPGAFEGVTVFHRIAEAKLTSVPKGLPP 240  
 DB 181 KVKIKQDFTKGMNALHVLMSANPLDNNNGIEPGAFEGVTVFHRIAEAKLTSVPKGLPP 240  
 QY 241 TLELHLDYNKISTVELEDFKRYKELQRLGLGNKKTIDENGLANIPRVREIHLNNKL 300  
 DB 241 TLELHLDYNKISTVELEDFKRYKELQRLGLGNKKTIDENGLANIPRVREIHLNNKL 300

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; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020132768A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020132768A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 2
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo Sapien

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US-09-945-015-2

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Query Match 100.0%; Score 1992; DB 10; Length 379;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKEYVLLFLALCSAKPFFSPSHALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDNSLPPTRE 60
Db 1 MKEYVLLFLALCSAKPFFSPSHALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDNSLPPTRE 60

QY 61 PRSHFFPDLFPMCPFCQCYSRVVHCSDGLTSVPTNIPFDTMRMLDLQNNKIKEIKEND 120
Db 61 PRSHFFPDLFPMCPFCQCYSRVVHCSDGLTSVPTNIPFDTMRMLDLQNNKIKEIKEND 120

QY 121 FKGLTSLYGLTLNNKLTTHPKAFLTQTKLRRLYLISHNOLSEIPLNPKSLAELRIHEN 180
Db 121 FKGLTSLYGLTLNNKLTTHPKAFLTQTKLRRLYLISHNOLSEIPLNPKSLAELRIHEN 180

QY 181 KVKKIQDTPKGMNALHVLMSANPLDNGIEPCAFEGVTVFHRITAEAKLTSPVKGGLPP 240
Db 181 KVKKIQDTPKGMNALHVLMSANPLDNGIEPCAFEGVTVFHRITAEAKLTSPVKGGLPP 240

QY 241 TLELHLHDYNNKISTVELEDFKRYKELQRLGLGNKNTIDIEGSLANIPRVREIHLNNKL 300
Db 241 TLELHLHDYNNKISTVELEDFKRYKELQRLGLGNKNTIDIEGSLANIPRVREIHLNNKL 300

QY 301 KKIPSGLPKLYLQIIFLHNSNARVGNDFCTVPKMKKSLYSATSLFNNPKYWMQOP 360
Db 301 KKIPSGLPKLYLQIIFLHNSNARVGNDFCTVPKMKKSLYSATSLFNNPKYWMQOP 360

QY 361 ATRFCVLSRMSVOLGNFGM 379
Db 361 ATRFCVLSRMSVOLGNFGM 379

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RESULT 14

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US-09-944-396-2
; Sequence 2, Application US/09944396
; Patent No. US20020132981A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavlin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548PICI
; CURRENT APPLICATION NUMBER: US/09/944,396
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330.
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999

```

APPLICANT: Baker, Kevin  
 APPLICANT: Botstein, David  
 APPLICANT: Eaton, Dan  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Gerritsen, Mary  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul  
 APPLICANT: Grimaldi, Christopher  
 APPLICANT: Gurney, Austin  
 APPLICANT: Hillan, Kenneth  
 APPLICANT: Kljavin, Ivar  
 APPLICANT: Napier, Mary  
 APPLICANT: Roy, Margaret  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Wood, William  
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 TYPE OF INVENTION: ACIDS ENCODING THE SAME  
 FILE REFERENCE: P2548p1c1  
 CURRENT APPLICATION NUMBER: US/09/944,097  
 CURRENT FILING DATE: 2001-08-31  
 PRIOR APPLICATION NUMBER: 09/866,028  
 PRIOR FILING DATE: 2001-05-25  
 PRIOR APPLICATION NUMBER: 60/069,334  
 PRIOR FILING DATE: December 11, 1997  
 PRIOR APPLICATION NUMBER: 60/069335  
 PRIOR FILING DATE: December 11, 1997  
 PRIOR APPLICATION NUMBER: 60/069,278  
 PRIOR FILING DATE: December 11, 1997  
 PRIOR APPLICATION NUMBER: 60/069,425  
 PRIOR FILING DATE: December 12, 1997  
 PRIOR APPLICATION NUMBER: 60/069,696  
 PRIOR FILING DATE: December 16, 1997  
 PRIOR APPLICATION NUMBER: 60/069,694  
 PRIOR FILING DATE: December 16, 1997  
 PRIOR APPLICATION NUMBER: 60/069,702  
 PRIOR FILING DATE: December 16, 1997  
 PRIOR APPLICATION NUMBER: 60/069,870  
 PRIOR FILING DATE: December 17, 1997  
 PRIOR APPLICATION NUMBER: 60/069,873  
 PRIOR FILING DATE: December 17, 1997  
 PRIOR APPLICATION NUMBER: 60/068,017  
 PRIOR FILING DATE: December 18, 1997  
 PRIOR APPLICATION NUMBER: 60/070,440  
 PRIOR FILING DATE: January 5, 1998  
 PRIOR APPLICATION NUMBER: 60/074,086  
 PRIOR FILING DATE: February 9, 1998  
 PRIOR APPLICATION NUMBER: 60/074,092  
 PRIOR FILING DATE: February 9, 1998  
 PRIOR APPLICATION NUMBER: 60/075,945  
 PRIOR FILING DATE: February 25, 1998  
 PRIOR APPLICATION NUMBER: 60/112,850  
 PRIOR FILING DATE: December 16, 1998  
 PRIOR APPLICATION NUMBER: 60/113,296  
 PRIOR FILING DATE: December 22, 1998  
 PRIOR APPLICATION NUMBER: 60/146,222  
 PRIOR FILING DATE: July 28, 1999  
 PRIOR APPLICATION NUMBER: PCT/US98/19330  
 PRIOR FILING DATE: September 16, 1998  
 PRIOR APPLICATION NUMBER: PCT/US98/25108  
 PRIOR FILING DATE: December 1, 1998  
 PRIOR APPLICATION NUMBER: 09/216,021  
 PRIOR FILING DATE: December 16, 1998  
 PRIOR APPLICATION NUMBER: 09/218,517  
 PRIOR FILING DATE: December 22, 1998  
 PRIOR APPLICATION NUMBER: 09/254,311  
 PRIOR FILING DATE: March 3, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/12252  
 PRIOR FILING DATE: June 22, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/21090  
 PRIOR FILING DATE: September 15, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/28409  
 PRIOR FILING DATE: No. US20020133675A1ember 30, 1999

RESULT 15  
 US-09-944-097-2  
 ; Sequence 2, Application US/09944097  
 ; Patent No. US20020133675A1  
 ; GENERAL INFORMATION:  
 ;  
 ; PRIOR APPLICATION NUMBER: PCT/US99/12252  
 ; PRIOR FILING DATE: June 22, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090  
 ; PRIOR FILING DATE: September 15, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28409  
 ; PRIOR FILING DATE: No. US20020133675A1ember 30, 1999







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; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 2
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-943-762-2

Query Match          100.0%; Score 1992; DB 10; Length 379;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDDSLPPTRE 60
Db 1 MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDDSLPPTRE 60

Qy 61 PRSHFFFDLPMPFCGQCYSRVVHCHSDGLTSVPTNIPFDTRMLDLQNNKIKEIKEND 120
Db 61 PRSHFFFDLPMPFCGQCYSRVVHCHSDGLTSVPTNIPFDTRMLDLQNNKIKEIKEND 120

Qy 121 FKGLTSLYGLILNNKLTJTKHPKAFLTTKLRLRLYLSHNSLSEIPLMLPKSLAELRIHEN 180
Db 121 FKGLTSLYGLILNNKLTJTKHPKAFLTTKLRLRLYLSHNSLSEIPLMLPKSLAELRIHEN 180

Qy 181 KVKIKQDTFKGMALHVLNSANPLDNGTEPGAFSGVTFVHRIAEAKLTSPVKGLPP 240
Db 181 KVKIKQDTFKGMALHVLNSANPLDNGTEPGAFSGVTFVHRIAEAKLTSPVKGLPP 240

Qy 241 TLLEHLHDYNNKISTVELEDFKRYKELQRLGLGNNKITTIDENGSLANIPTVRYREIHLNNKL 300
Db 241 TLLEHLHDYNNKISTVELEDFKRYKELQRLGLGNNKITTIDENGSLANIPTVRYREIHLNNKL 300

Qy 301 KKIISGLPELYLQIIFLHNSIARVGVNDPCTPTPKMKKSLYSALSFLNPNKYWEMQP 360
Db 301 KKIISGLPELYLQIIFLHNSIARVGVNDPCTPTPKMKKSLYSALSFLNPNKYWEMQP 360

Qy 361 ATRFCVLSRMSVOLGNFCM 379
Db 361 ATRFCVLSRMSVOLGNFCM 379

RESULT 18
US-09-944-654-2
; Sequence 2, Application US/09944654
; Patent No. US20020142959A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tamas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,654
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020142959A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020142959A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000

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[illegible]

Db 331 ISXTSIPDMYECIRXANEVTL 352

RESULT 22

US-10-028-072-302

Sequence 302, Application US/10028072

Publication No. US20030004311A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: DeForge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William

APPLICANT: Zhang

TITLE OF INVENTION:

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/028, 072

CURRENT FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/049911

PRIOR FILING DATE: 1997-06-18

PRIOR APPLICATION NUMBER: 60/056974

PRIOR FILING DATE: 1997-08-26

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059115

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059117

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059122

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059184

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059263

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/059352

PRIOR FILING DATE: 1997-09-19

PRIOR APPLICATION NUMBER: 60/059588

PRIOR FILING DATE: 1997-09-19

PRIOR APPLICATION NUMBER: 60/059836

PRIOR FILING DATE: 1997-09-24

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/062285

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/062287

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/062814

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/062816

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/063045

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/063082

PRIOR FILING DATE: 1997-10-31

PRIOR APPLICATION NUMBER: 60/063127

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/063327

PRIOR FILING DATE: 1997-10-27

PRIOR APPLICATION NUMBER: 60/063329

PRIOR FILING DATE: 1997-10-27

PRIOR APPLICATION NUMBER: 60/063550

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/063561

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/063704

PRIOR FILING DATE: 1997-10-29

PRIOR APPLICATION NUMBER: 60/063733

PRIOR FILING DATE: 1997-10-29

PRIOR APPLICATION NUMBER: 60/063735

PRIOR FILING DATE: 1997-10-29

PRIOR APPLICATION NUMBER: 60/063738

PRIOR FILING DATE: 1997-10-29

PRIOR APPLICATION NUMBER: 60/063755

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064248

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/064809

PRIOR FILING DATE: 1997-11-07

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065846

PRIOR FILING DATE: 1997-11-17

PRIOR APPLICATION NUMBER: 60/066364

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/066453

PRIOR FILING DATE: 1997-11-24

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PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/069212

PRIOR FILING DATE: 1997-12-11

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PRIOR FILING DATE: 1997-12-11

PRIOR APPLICATION NUMBER: 60/069334

PRIOR FILING DATE: 1997-12-11

PRIOR APPLICATION NUMBER: 60/069694

PRIOR FILING DATE: 1997-12-16

PRIOR APPLICATION NUMBER: 60/072320

PRIOR FILING DATE: 1998-01-23

PRIOR APPLICATION NUMBER: 60/073612

PRIOR FILING DATE: 1998-02-04

PRIOR APPLICATION NUMBER: 60/074086

PRIOR FILING DATE: 1998-03-09

PRIOR APPLICATION NUMBER: 60/074092

PRIOR FILING DATE: 1998-02-09

PRIOR APPLICATION NUMBER: 60/077791

PRIOR FILING DATE: 1998-03-12

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/079294

PRIOR FILING DATE: 1998-03-25

PRIOR APPLICATION NUMBER: 60/079663

PRIOR FILING DATE: 1998-02-27

PRIOR APPLICATION NUMBER: 60/079728

PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: 60/080165

PRIOR FILING DATE: 1998-03-31

PRIOR APPLICATION NUMBER: 60/081203

PRIOR FILING DATE: 1998-04-09

PRIOR APPLICATION NUMBER: 60/081229

PRIOR FILING DATE: 1998-04-09

PRIOR APPLICATION NUMBER: 60/081695

PRIOR FILING DATE: 1998-04-14

PRIOR APPLICATION NUMBER: 60/081817

PRIOR FILING DATE: 1998-04-15

PRIOR APPLICATION NUMBER: 60/081818

PRIOR FILING DATE: 1998-04-15

PRIOR APPLICATION NUMBER: 60/082999

PRIOR FILING DATE: 1998-04-24

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/083545

PRIOR FILING DATE: 1998-04-29



PRIOR FILING DATE:	1998-04-09
PRIOR APPLICATION NUMBER:	60/081695
PRIOR FILING DATE:	1998-04-14
PRIOR APPLICATION NUMBER:	60/081817
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/081818
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PRIOR FILING DATE:	1998-05-12
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PRIOR FILING DATE:	1998-05-13
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PRIOR FILING DATE:	1998-05-13
PRIOR APPLICATION NUMBER:	60/085339
PRIOR FILING DATE:	1998-05-13
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PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085697
PRIOR FILING DATE:	1998-05-15
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PRIOR APPLICATION NUMBER:	60/086414
PRIOR FILING DATE:	1998-05-22
PRIOR APPLICATION NUMBER:	60/086430
PRIOR FILING DATE:	1998-05-22
PRIOR APPLICATION NUMBER:	60/087106
PRIOR FILING DATE:	1998-05-28
PRIOR APPLICATION NUMBER:	60/088026
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088730
PRIOR FILING DATE:	1998-06-10
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PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088810
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088858
PRIOR FILING DATE:	19/98-06-11
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PRIOR FILING DATE:	1998-06-17
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PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089907
PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	60/089947
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/090349
PRIOR FILING DATE:	1998-06-23
PRIOR APPLICATION NUMBER:	60/090429
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090445
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090538
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090863
PRIOR FILING DATE:	1998-06-26
PRIOR APPLICATION NUMBER:	60/091360
PRIOR FILING DATE:	1998-07-01
PRIOR APPLICATION NUMBER:	60/091519
PRIOR FILING DATE:	1998-07-02
PRIOR APPLICATION NUMBER:	60/091982
PRIOR FILING DATE:	1998-07-02



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Query Match      18.2%; Score 363.5; DB 9; Length 674;
Best Local Similarity 32.7%; Pred. No. 9.1e-23;
Matches 92; Conservative 51; Mismatches 105; Indels 33; Gaps 7;

QY 74 CPGCQCYSRVVHCSDGLTSVPTNIPDTRMLDQNNKKEIKENDFKGLTSLYGLILN 133
Db 54 CFSVCRCDNGFIYCNDRGLTSIPAIDPDATTLYLQNNQI-----N 94

QY 134 NKLTKIHPKAFLTTKLRRLYLSHNQLSEITPLNPKSLAEIRHENKVKIKQDTPFGM 193
Db 95 NAGI-----PSDLKLLKVERIYHNSLDEFTPLNPKYKELHLQENNTIYDSLSKI 150

QY 194 NALHVLMSANPLDNGIEPGAF-EGVTVFHIRIAEAKLTSVPKGLPTLLEHLHDYDKI 252
Db 151 PLEELHDDNSVSAVSEIEGAFSDSKLFLSRNHLSTIPGSLPHTLEELRLDDNRI 210

QY 253 STVELEDFKRYKELQRLGLGNKTIENGSLANIIPRVREIHLNENKIKIPSGLP 310
Db 211 STIPLHAFKGLNSLRRLVLDGNNLANQRIADDTFSLQNLTELSLYRNSLAAPNLNPS- 269

QY 311 KYLQIIFLHNSIARVGVNDPCTVPKMKSLYSALSIFNN 351
Db 270 AHLQKLYLQDINAISHIPYN---TLAKMRE--LERLDLSNN 304

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RESULT 24
US-09-764-870-276
; Sequence 276, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PZ14
; CURRENT APPLICATION NUMBER: US/09764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 276
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-870-276

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Query Match      16.6%; Score 331.5; DB 10; Length 623;
Best Local Similarity 33.0%; Pred. No. 3.9e-20;
Matches 86; Conservative 37; Mismatches 111; Indels 27; Gaps 5;

QY 74 CPGCQCYSRVVHCSDGLTSVPTNIPDTRMLDQNNKKEIKENDFKGLTSLYGLILN 133
Db 5 CFSVCRCDNGFIYCNDRGLTSIPAIDPDATTLYLQNNQI-----N 45

QY 134 NKLTKIHPKAFLTTKLRRLYLSHNQLSEITPLNPKSLAEIRHENKVKIKQDTPFGM 193
Db 46 NAGI-----PSDLKLLKVERIYHNSLDEFTPLNPKYKELHLQENNTIYDSLSKI 101

QY 194 NALHVLMSANPLDNGIEPGAFEGVTVFHIR-IAEAKLTSVPKGLPTLLEHLHDYDKI 252
Db 102 PLEELHDDNSVSAVSEIEGAFSDSKLFLSRNHLSTIPGSLPHTLEELRLDDNRI 161

QY 253 STVELEDFKRYKELQRLGLGNKTIENGSLANIIPRVREIHLNENKIKIPSGLP 310
Db 162 STISSPSLQGLTSKLRLVLDGNNLHGLGDKVFFNLVNLTELSLYRNSLAAPVNLPGT 221

QY 311 KYLQIIFLHNSIARVGVNDP 331
Db 222 N-LRKLYLQDNIHNRVPPNAF 241

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RESULT 25
US-10-063-547-132
; Sequence 132, Application US/10063547

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; Publication No. US20020182638A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,547
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 132
; LENGTH: 649
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-063-547-132

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Query Match      16.6%; Score 331.5; DB 9; Length 649;
Best Local Similarity 33.0%; Pred. No. 4.1e-20;
Matches 86; Conservative 37; Mismatches 111; Indels 27; Gaps 5;

QY 74 CPGCQCYSRVVHCSDGLTSVPTNIPDTRMLDQNNKKEIKENDFKGLTSLYGLILN 133
Db 31 CFSVCRCDNGFIYCNDRGLTSIPAIDPDATTLYLQNNQI-----N 71

QY 134 NKLTKIHPKAFLTTKLRRLYLSHNQLSEITPLNPKSLAEIRHENKVKIKQDTPFGM 193
Db 72 NAGI-----PSDLKLLKVERIYHNSLDEFTPLNPKYKELHLQENNTIYDSLSKI 127

QY 194 NALHVLMSANPLDNGIEPGAFEGVTVFHIR-IAEAKLTSVPKGLPTLLEHLHDYDKI 252
Db 128 PLEELHDDNSVSAVSEIEGAFSDSKLFLSRNHLSTIPGSLPHTLEELRLDDNRI 187

QY 253 STVELEDFKRYKELQRLGLGNKTIENGSLANIIPRVREIHLNENKIKIPSGLP 310
Db 188 STISSPSLQGLTSKLRLVLDGNNLHGLGDKVFFNLVNLTELSLYRNSLAAPVNLPGT 247

QY 311 KYLQIIFLHNSIARVGVNDP 331
Db 248 N-LRKLYLQDNIHNRVPPNAF 267

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RESULT 26
US-10-004-551-6
; Sequence 6, Application US/10004551
; Publication No. US20030004310A1
; GENERAL INFORMATION:
; APPLICANT: SHIMKETS, RICHARD A
; APPLICANT: FERNANDES, ELMA
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
; FILE REFERENCE: 15966-559
; CURRENT APPLICATION NUMBER: US/10/004,551
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 09/635,949
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 649
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-004-551-6

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Query Match      16.6%; Score 331.5; DB 9; Length 649;
Best Local Similarity 33.0%; Pred. No. 4.1e-20;
Matches 86; Conservative 37; Mismatches 111; Indels 27; Gaps 5;

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Db      248 N-LRKLYLQDNHINRVPNNAF 267

RESULT 28
US-10-176-758-384
; Sequence 384, Application US/10176758
; Publication No. U520030008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEOTIDE SEQUENCES ENCODING THE SAME
; FILE REFERENCE: P343ORIC104
; CURRENT APPLICATION NUMBER: US/10/176,758
; PRIOR FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 384
; LENGTH: 649
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-758-384

Query Match          16.6%; Score 331.5; DA 9; Length 649;
Best Local Similarity 33.0%; Pred.No.4.1e-20;
Matches    86; Conservative   37; Mismatches 111; Indels     27; Gaps

QY  74 CPFCQCYSRVHCSDGLGTSVPTNPFDTRMLDLQNKKIKEIKENDFKGLTSLYLGIILN 133
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DB  31 CPSVCRCDAFIYCNDREFLTSIPTGPEDATTLYLQQNQI-----N 71

QY  134 NNKTKTHPKAFLLTTKLRLYLSHNSOLSEPLNLPSLAELRIHENKYVKIQDTEFGM 193
       | :| :| :| :|| | || | || | || | || | || | || | || | || | ||
DB  72 NAGT----PSDLKNLLKVREYYLIYHSLSDEFFPNLRPVKEQLHQNNIRITYDSLSKI 127

QY  194 NALHVLEMSANPLDDNGNIIEPCAGEGVTVFHIR-IARAKLTSVBKGLPPTLLELDYDKI 252
       || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB  128 PYLEEHLDDNSVSAYSIESGAFRDSNYLLRFLESRNHLSTIPWGLPRTEEELRLDDNR 187

QY  253 STVELEDFEKKYEKLORLGLNKNTIDENG--LANTPRVREIHLENKCLKKTSPSGLPEL 310
       || :| :| :| :|| | || | || | || | || | || | || | || | || | ||
DB  188 STISPSLOGLTSLKRVLVDGNLINNHGLGDVFVNLVNLTSELVRNSLTAAAPVNLPGT 247

QY  311 KYLQIIIFLHNSIARGVWNDF 331
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DB  248 N-LRKLYLQDNHINRVPNNAF 267


RESULT 29
US-10-063-616-132
; Sequence 132, Application US/10063616
; Publication No. U520030013855A1
; GENERAL INFORMATION:
; APPLICANT: Eaton,Dan L.
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,Christopher J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEOTIDE SEQUENCES ENCODING THE SAME
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; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 132
; LENGTH: 649
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-063-616-132

Query Match 16.6%; Score 331.5; DB 9; Length 649;
Best Local Similarity 33.0%; Pred. No. 4.1e-20;
Matches 86; Conservative 37; Mismatches 111; Indels 27; Gaps 5;

QY 74 CPFGCQCYRVVHCSDLGTSVPTNPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
DB 31 CPSCVRCDCAGFIYCNDRFLTSIPTGIPEDATTLTLQNNQI-----N 71

QY 134 NKKLTKIHPKAFLTTKLRLRLYLSHNSLSEIPLNPKSLAELRIHENKVKKIQKDTFKGM 193
DB 72 NAGI-----PSDLKLLKVERIYLYHNSLDEFTNLPKYVKELHLOENIRITYDSLSKI 127

QY 194 NALHVLEMSANPLDNNNGIEPGAFEGTVVFHIR-IAEAKLTSPKGLPPTLLEHLHDYDKI 252
DB 128 PYLEELHLDNDSVSAVSIEEGAFRDSNYLRLFLSRNHLSTIPWGLPRTIEELRLDDNRI 187

QY 253 STVELEDFKRYKELQRLGLGNKKTIDTENG--LANIPRVREIHLNKKKIPSGLP 310
DB 188 STISSPSLQGLTSLKRLVLDGNNHGLGDKVFFNLVNLTELSLVRNSLTAAPVNLPGT 247

QY 311 KYLOIIFLHNSIARVGVNDF 331
DB 248 N-LRKLYLQDNHINRVPNAP 267

RESULT 31
US-10-006-867-132
; Sequence 132, Application US/10006867
; Patent No. US20020119130A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/006,867
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/063435
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/064215
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
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; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089952

QY 74 CPFGCQCYRVVHCSDLGTSVPTNPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
DB 31 CPSCVRCDCAGFIYCNDRFLTSIPTGIPEDATTLTLQNNQI-----N 71

QY 134 NKKLTKIHPKAFLTTKLRLRLYLSHNSLSEIPLNPKSLAELRIHENKVKKIQKDTFKGM 193
DB 72 NAGI-----PSDLKLLKVERIYLYHNSLDEFTNLPKYVKELHLOENIRITYDSLSKI 127

QY 194 NALHVLEMSANPLDNNNGIEPGAFEGTVVFHIR-IAEAKLTSPKGLPPTLLEHLHDYDKI 252
DB 128 PYLEELHLDNDSVSAVSIEEGAFRDSNYLRLFLSRNHLSTIPWGLPRTIEELRLDDNRI 187

QY 253 STVELEDFKRYKELQRLGLGNKKTIDTENG--LANIPRVREIHLNKKKIPSGLP 310
DB 188 STISSPSLQGLTSLKRLVLDGNNHGLGDKVFFNLVNLTELSLVRNSLTAAPVNLPGT 247

QY 311 KYLOIIFLHNSIARVGVNDF 331
DB 248 N-LRKLYLQDNHINRVPNAP 267

RESULT 30
US-10-175-737-384
; Sequence 384, Application US/10175737
; Publication No. US20030013153A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C50
; CURRENT APPLICATION NUMBER: US/10/175,737
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
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; LENGTH: 649
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-175-737-384

Query Match 16.6%; Score 331.5; DB 9; Length 649;
Best Local Similarity 33.0%; Pred. No. 4.1e-20;
Matches 86; Conservative 37; Mismatches 111; Indels 27; Gaps 5;

QY 74 CPFGCQCYRVVHCSDLGTSVPTNPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
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; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
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; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089908

Query Match      16.6%; Score 331.5; DB 12; Length 649;
Best Local Similarity 33.0%; Pred. No. 4.le-20;
Matches 86; Conservative 37; Mismatches 111; Indels 27; Gaps 5;

QY 74 CPEGCCQYSRVVHCDLGLTSVPTNIPDTRMLDQNNKIKEIKENDFKGLTSLYGLILN 133
DB 31 CFSVCRCDAGFYICNDRLFISPTIGIPEDATTLYLQNNQI-----N 71

QY 134 NNKLTKEIHPKAFLTTKLRLRYLSHNSQLSEIPLNLPKSLAELRIHENKVKXIOKDTFKGM 193
DB 72 NAGI---PSDLKNLLKVERIYLYHNSLDEPPTNLPKYVKELHLQENNIRITTYDSLKI 127

QY 194 NALHVLMSANPLDNNGIEPGAFEGVTVFHIR-IAEAKLTSPKGLPPTILLELHLDYANKI 252
DB 128 PYLEELHLDNDSVSAVSIEBEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEBLRDDNRI 187

QY 253 STVELEDFKRYKELQRLGLGNKKITDIENG--LANIPRVREIHLNENKKKIPSGLPPEL 310
DB 188 STISSPSLQGLTSLKRLVLDGNLNNHGLGDKVFFENLVNLTLSLVRNSLTAAAPVNLPGT 247

QY 311 KYLOIFLHNSIARVGNDF 331
DB 248 N-LRKLYLQDNHINRVPPNAF 267

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RESULT 33
US-10-028-072-370
; Sequence 370, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028,072
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
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7	PRIOR FILING DATE: 1998-02-09	
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7	PRIOR APPLICATION NUMBER: 60/082999	
7	PRIOR FILING DATE: 1998-04-24	
7	PRIOR APPLICATION NUMBER: 60/083222	
7	PRIOR FILING DATE: 1998-04-28	
7	PRIOR APPLICATION NUMBER: 60/083545	
7	PRIOR FILING DATE: 1998-04-29	
7	PRIOR APPLICATION NUMBER: 60/084600	
7	PRIOR FILING DATE: 1998-05-07	
7	PRIOR APPLICATION NUMBER: 60/084627	
7	PRIOR FILING DATE: 1998-05-07	
7	PRIOR APPLICATION NUMBER: 60/084637	
7	PRIOR FILING DATE: 1998-05-07	
7	PRIOR APPLICATION NUMBER: 60/085149	
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7	PRIOR FILING DATE: 1998-05-13	
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7	PRIOR FILING DATE: 1998-05-13	
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7	PRIOR FILING DATE: 1998-05-13	
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7	PRIOR FILING DATE: 1998-05-15	
7	PRIOR APPLICATION NUMBER: 60/085697	
7	PRIOR FILING DATE: 1998-05-15	
7	PRIOR APPLICATION NUMBER: 60/085704	
7	PRIOR FILING DATE: 1998-05-15	
7	PRIOR APPLICATION NUMBER: 60/086414	
7	PRIOR FILING DATE: 1998-05-22	
7	PRIOR APPLICATION NUMBER: 60/086430	
7	PRIOR FILING DATE: 1998-06-04	
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7	PRIOR FILING DATE: 1998-06-10	
7	PRIOR APPLICATION NUMBER: 60/088741	
7	PRIOR FILING DATE: 1998-06-10	
7	PRIOR APPLICATION NUMBER: 60/088810	
7	PRIOR FILING DATE: 1998-06-10	
7	PRIOR APPLICATION NUMBER: 60/088858	
7	PRIOR FILING DATE: 19/98-06-11	
7	PRIOR APPLICATION NUMBER: 60/089532	
7	PRIOR FILING DATE: 1998-06-17	
7	PRIOR APPLICATION NUMBER: 60/089599	
7	PRIOR FILING DATE: 1998-06-17	
7	PRIOR APPLICATION NUMBER: 60/089907	
7	PRIOR FILING DATE: 1998-06-18	

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; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090538
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07

Query Match      16.5%; Score 329; DB 9; Length 642;
Best Local Similarity 29.1%; Pred. No. 6.6e-20;
Matches 98; Conservative 55; Mismatches 146; Indels 38; Gaps 9;

QY 51 EDNSLFTPTREPSHFPPDLP-----MCPFGCQCYSR-VVHCSDLGLTSVPTNIPDTR 104
DB 70 EENE-FAEEEPVVLSPPEPGGPAAYSCPRDCACSQGVVDCGGIDLREFPGDLPEHTN 128
QY 105 MLDLQNNKIKIKENDFKGLTSVGLTLNKNKLT--IHPKATLTTKRLRLYSHNOLS 162
DB 129 HLSLQNNQLEKIYPEELSRHLRLETLNQNRLTSRGLPEKAHEHTLNLYLANNKLT 188
QY 163 EIPNLKPSLAELRIHENKVKIKQDFTFGMNAHLVLEMSANPLDNNNGIEPGAFEGVTVF 222
DB 189 LAPRFLNALISVDFAAANYLTIKYGLTFGOKPNLRSVYLHNNKLADAGLDNNMGSSNV 248
QY 223 HIRTAEK-LTSVPKGLPPTLLEHLHDYKNISTVELEDFRKYRELQRLGNNKITYD--I 279
DB 249 EVLILSSNLRHVPHKLPALYKILHKNKLEKIPPGAFSELSSRLRYLQNNYLTDEGL 308
QY 280 ENGLANIPRVRETHLENNKIKTPSGLP-----LKYLQIIF 317
DB 309 DNETFWKLSLEYLDLSNNLSRVPAGLPSRLVLLHLEKNAIRSVANVLTPIRSLEYLL 368
QY 318 LHSNIAVGVNDPCTVPKMKKSLYSALSLFNPNVK 354
DB 369 LHSNQLREQGIH---PLAFQGLKRLHT-VHLYNNALE 401

RESULT 34
US-09-925-301-1192
; Sequence 1192, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1192
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (11)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE

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; LOCATION: (13)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1192

Query Match      16.2%; Score 323; DB 10; Length 415;
Best Local Similarity 26.4%; Pred. No. 1.2e-19;
Matches 87; Conservative 64; Mismatches 131; Indels 48; Gaps 9;

QY 63 SHEFPPDLFPM-----CPFGCOC---YSRVVHCSDLG 91
DB 76 TTYIDYDYPYETYPYGYGVDEGPAYTYGSPSPDPDCQECPPNFPTAMTCDDRN 135
QY 92 LTSVPTNIPFTRMLDLQNNKIKIKENDFKGLTSVGLTLNKNKLT--KIHPKAFLTTK 149
DB 136 LAYLPP-VPSRMKYVYFQNNQITSIQEGVDNATGLLWALHGNQITSDKVGKRVFSKLR 194
QY 150 KLRRLYSHNQLSEIPLNPKSLAEIRIHENKVKIKQDFTFGMNAHLVLEMSANPLDNN 209
DB 195 HLERLYLDHNNLTRMPGLPLRSLRELHLDHNOISRVPNNALEGLENLALYLOHNEIOEV 254
QY 210 GIEPGAFEGV-TVFHIRTAEAKLTSVPKGLPPTLLEHLHDYKNISTVELEDFKRYKELOR 268
DB 255 G---SSMRGLRSLIILDLUSYNHLRKPDPGLPSALEQLWMEHNNVTVPDSYFRGAPKLLY 311
QY 269 LGLGNKTKTDIENGSLA----NIPRVRETHLENNKIKIPSPOLPELYLIQIFLHNSIA 324
DB 312 VRLSHNSLT---NGLASNTFNSSSLLELDLSYNQLQKIP---PVNTNLENLYLQGNRIN 365
QY 325 RVGVNDFCTVPKMKKSLYSALSLFNPNVK 354
DB 366 EFSISFCTVVDVNVFSLQVLRLDGNIEK 395

RESULT 35
US-09-905-201A-28
; Sequence 28, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698

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; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 28
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-291A-28

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Query Match      15.7%; Score 313.5; DB 9; Length 660;
Best Local Similarity 27.7%; Pred. No. 1.4e-18;
Matches 79; Conservative 62; Mismatches 109; Indels 35; Gaps 8;

QY 74 CPGGOCYSRVVHCSDGLTSTVPNIPDTRMLDLQNNKKEIKENDFKGLTSLYGLILN 133
Db 36 CFSVCRCDRNFVNCNERSLTSVPLGIP-----EGVTVLY---LH 71

QY 134 NKLTKI-HPKAFLTTKRLRLYLHSHNOLSEIPLNPKSLAELRIHENKVKIKOKDFKG 192
Db 72 NNQINNAGFPAELHNVQSVHTVLYGNQDDEFPMNLKPNVVLHLQENNQTISRALAQ 131

QY 193 MNALHVLMSANPLDNGNIGPGAF-EGVTVPFHIRIAEAKLTSPKGLPPTLLEHLHDYNK 251
Db 132 LKLEELHLDNDSISTGVGEDGAFREATISLKLFLSKNHLSSVPVGLPVDLQELRVDENR 191

QY 252 ISTVELEDFKRYKELQRLGLGNKKTID--IENGSLANTIPRVRETHLENNKIKKTPSGIPE 309
Db 192 IAVISDMAFQNLTSUERIVDGNLLTNKGTAEGTFSHLTKLKEFSIVRNSLSLHPPDLP 251

QY 310 LKYLIQIIFHNSIARVGVDNFCPTVPKMKKSLYSALSIFNNPVK 354
Db 252 THLIR-LYLDQNIQHIIPLTAF-SNLARKLER-----LDISNNQLR 289

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RESULT 36
US-10-066-500-115
; Sequence 115, Application US/10066500
; Patent No. US2002017165A1
; GENERAL INFORMATION:
; APPLICANT: AVI J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Bolstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong

```

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; APPLICANT: Wei-Oiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P. Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3130R1C7
; CURRENT APPLICATION NUMBER: US/10/066,500
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 10/002,796
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
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; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101922
; PRIOR FILING DATE: 1998-09-24

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;; PRIOR APPLICATION NUMBER: 60/106032  
;; PRIOR FILING DATE: 1998-10-28  
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;; PRIOR APPLICATION NUMBER: 60/125778  
;; PRIOR FILING DATE: 1999-03-23  
;; PRIOR APPLICATION NUMBER: 60/139695  
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;; PRIOR FILING DATE: 1999-07-20  
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;; PRIOR APPLICATION NUMBER: 60/149396  
;; PRIOR FILING DATE: 1999-08-17  
;; PRIOR APPLICATION NUMBER: 60/169495  
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;; PRIOR FILING DATE: 1997-09-19  
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;; PRIOR APPLICATION NUMBER: 09/136801  
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;; PRIOR FILING DATE: 1998-08-19  
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;; PRIOR FILING DATE: 1998-12-08  
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;; PRIOR FILING DATE: 1999-03-03  
;; PRIOR APPLICATION NUMBER: 09/254460  
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;; PRIOR APPLICATION NUMBER: 09/284663  
;; PRIOR FILING DATE: 1999-04-15  
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;; PRIOR APPLICATION NUMBER: 09/664610  
;; PRIOR FILING DATE: 2000-09-18  
;; PRIOR APPLICATION NUMBER: 09/665350

;; PRIOR FILING DATE: 2000-09-18  
;; PRIOR APPLICATION NUMBER: 09/709238  
;; PRIOR FILING DATE: 2000-11-08  
;; PRIOR APPLICATION NUMBER: 09/767609  
;; PRIOR FILING DATE: 2001-01-22  
;; PRIOR APPLICATION NUMBER: 09/802706  
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;; PRIOR APPLICATION NUMBER: 09/866028  
;; PRIOR FILING DATE: 2001-05-25  
;; PRIOR APPLICATION NUMBER: 09/870574  
;; PRIOR FILING DATE: 2001-05-30  
;; PRIOR APPLICATION NUMBER: 09/872035  
;; PRIOR FILING DATE: 2001-06-01  
;; PRIOR APPLICATION NUMBER: 09/886342  
;; PRIOR FILING DATE: 2001-06-19  
;; PRIOR APPLICATION NUMBER: PCT/US98/14552  
;; PRIOR FILING DATE: 1998-07-14  
;; PRIOR APPLICATION NUMBER: PCT/US98/18824  
;; PRIOR FILING DATE: 1998-09-10  
;; PRIOR APPLICATION NUMBER: PCT/US98/19093  
;; PRIOR FILING DATE: 1998-09-14  
;; PRIOR APPLICATION NUMBER: PCT/US98/19330  
;; PRIOR FILING DATE: 1998-09-16  
;; PRIOR APPLICATION NUMBER: PCT/US98/19437  
;; PRIOR FILING DATE: 1998-09-17  
;; PRIOR APPLICATION NUMBER: PCT/US98/24855  
;; PRIOR FILING DATE: 1998-11-20  
;; PRIOR APPLICATION NUMBER: PCT/US98/25108  
;; PRIOR FILING DATE: 1998-12-01  
;; PRIOR APPLICATION NUMBER: PCT/US98/25190  
;; PRIOR FILING DATE: 1998-11-25  
;; PRIOR APPLICATION NUMBER: PCT/US99/05028  
;; PRIOR FILING DATE: 1999-03-08  
;; PRIOR APPLICATION NUMBER: PCT/US99/12252  
;; PRIOR FILING DATE: 1999-06-02  
;; PRIOR APPLICATION NUMBER: PCT/US99/20111  
;; PRIOR FILING DATE: 1999-09-01  
;; PRIOR APPLICATION NUMBER: PCT/US99/20594  
;; PRIOR FILING DATE: 1999-09-08  
;; PRIOR APPLICATION NUMBER: PCT/US99/21090  
;; PRIOR FILING DATE: 1999-09-15  
;; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 15.7%; Score 313.5; DB 9; Length 660;

Best Local Similarity 27.7%; Pred No. 1.4e-18;

Matches 79; Conservative 62; Mismatches 109; Indels 35; Gaps 8;

QY 74 CPGCQCYSRVVHCSDGLTSVPTNIPFTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133

Db 36 CFSVCRCDRNFVVCNERSLTSVPLGIP-----EGVTVLY---LH 71

QY 134 NNKLTKI-HPKAFLETKKLRRLYLSHNQSLSEIPLNPKSLAELRIHENKVKKIQKDTFG 192

Db 72 NNQINNAGFPaelhNVQSVHTVLYGNQLDEFPNMLPKNRVRLHLENNIQTISRAALAQ 131

QY 193 MNALHVLEMSANPLDNNNGIEGAF-EGVTVFHTRIAEAKLTSPKGLPPTLLELHLDYNK 251

Db 132 LKLELHLDNDSISTGVGEDGAFRAISLKLFLSKNHLSSVPVGLPVDLQELRVENR 191

QY 252 ISTVELEDFKRYKEQLRGLGNKKTID--TENGSLANIPRVREIHLNENKLIKIPSGLPE 309

Db 192 IAVISDMAFQNTLSERLIYDGNLLTNKGIAEGTFSHTLTKKEFSIVRNSLSHPPDLPG 251

QY 310 LKYLQILFLHSNSIARVGVNDFCPTVPKMKSLYSALSIFNNPVK 354

Db 252 THLIR-LYLQDNOINHIPTAF-SNLRKLER-----LDISNNQLR 289

RESULT 37

US-09-902-853-28

; Sequence 28, Application US/09902853

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; Publication No. US200020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 28
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-902-853-28

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Query Match 15.7%; Score 313.5; DB 9; Length 660;
Best Local Similarity 27.7%; Pred. No. 1.4e-18;
Matches 79; Conservative 62; Mismatches 109; Indels 35; Gaps 8;

QY 74 CPFGCCQYRVHVCSDIGLTSVPTNIPFDTRMLDLQNNKIKEKDNDFKGLTSLYGLILN 133
   || || || || || || || || || || || || || || || || || || || || ||
Db 36 CPVSCRCDRNFVYCNERSLTSVPLGIP-----EGVTVLY---LH 71
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QY 134 NNKLTKI-HPKAFLLTKRLRLYLSHNQLSEIPLNPKSLAEIRIHENKVKIKQDTFKG 192
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Db 72 NNQINNAGFAELHNVQSVHTVLYQNLDFEPNNLPKNVRLHLOENNIQIISRALAQ 131
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QY 193 MNALHVLMSANPLDNNGIEPGAF-EGVTVEHIRIAEAKLTSVPKGLPPTLLEHLHDYNK 251
   || || || || || || || || || || || || || || || || || || || || ||
Db 132 LLKLEELHDDNSISITGVGDEGAFRAISKLFLSKNHLSSVPGVLPVDQLRLVDENR 191
   || || || || || || || || || || || || || || || || || || || || ||

QY 252 ISTVELEDFKRYKELQRLGLGNKKTID--TENGSLANIPRVREIHLNENKLLKIPSGLPE 309
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Db 192 IAVISDMAFQNLTSLERLIVDGNLLTKNGIAEGTFSHLTKLKEFSIVRNSLSHPPDLPFG 251
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QY 310 LKYLQIIFLHSNSIARVGNDFCPTVPKMKKSLYSALISLENPNVK 354
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Db 252 THLIR-LYLDQNIHPIPTAF-SNLKLER-----LDISNNQLR 289
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RESULT 38
US-09-907-824-28
; Sequence 28, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,824
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944

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APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: ROY, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tunes, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/907,841  
PRIOR FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
REMAINING OF SEQ ID NOS: 423  
SEQUENCE OF SEQ ID NOS: 423  
LENGTH: 660  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-907-841-28

Query Match 15.7%; Score 313.5; DB 9; Length 660;  
Best Local Similarity 27.7%; Pred. No. 1.4e-18;  
Matches 79; Conservative 62; Mismatches 109; Indels 35; Gaps 8;  
Qy 74 CPFGCOCYRVVHCSDLGTSVPTNIPDTRMLDLQNNKIKEIKENDFKGLTSYGLILN 133  
Db 36 CPSVCRDRNFVYCNERSLTSVPLGIP-----EGVTVLV---LH 71  
Qy 134 NKLTKI-HPKAFLTTKRLRLYLSHNQLSEIPLNPKSLAELRIHENKVKIKQKDTFG 192  
Db 72 NNQINNAGFPAELHNVQSVHTVLYGNQDLDEFPNLPKNRVVLHLOENNIQTISRAALQ 131  
Qy 193 MNALHVLMSANPLDNGIEPGAF-EGVTVFHRIAEAKLTSPKGLPTLLELHDYKN 251  
Db 132 LKLEELHLDNDSITGVGEDGAFREAIKLLFLSKNHLSSVPVGLPVDQLRLVDENR 191  
Qy 252 ISTVELEDFRYKELQRLGLGNKKTID--IENGSLANIPRVREIHLNKKIKPSGLPE 309  
Db 192 IAVSDMAFQNLTSERLIVDGNLLTNKGAEGTFSHLTKKEFSIYVNSLSHPPDPLG 251  
Qy 310 LKYLQIIFLHNSIARVGVNDPCPTVPKMKKSLYSALSIFNNPVK 354  
Db 252 THLIR-LYLODNQINHIPLTAF-SNLRKLER-----LDISNNQLR 289

RESULT 39  
US-09-907-841-28  
Sequence 28, Application US/09907841  
Publication No. US20020198366A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: ROY, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tunes, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/907,841  
PRIOR FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
REMAINING OF SEQ ID NOS: 423  
SEQUENCE OF SEQ ID NOS: 423  
LENGTH: 660  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-907-841-28

Query Match 15.7%; Score 313.5; DB 9; Length 660;  
Best Local Similarity 27.7%; Pred. No. 1.4e-18;  
Matches 79; Conservative 62; Mismatches 109; Indels 35; Gaps 8;  
Qy 74 CPFGCOCYRVVHCSDLGTSVPTNIPDTRMLDLQNNKIKEIKENDFKGLTSYGLILN 133  
Db 36 CPSVCRDRNFVYCNERSLTSVPLGIP-----EGVTVLV---LH 71  
Qy 134 NKLTKI-HPKAFLTTKRLRLYLSHNQLSEIPLNPKSLAELRIHENKVKIKQKDTFG 192  
Db 72 NNQINNAGFPAELHNVQSVHTVLYGNQDLDEFPNLPKNRVVLHLOENNIQTISRAALQ 131  
Qy 193 MNALHVLMSANPLDNGIEPGAF-EGVTVFHRIAEAKLTSPKGLPTLLELHDYKN 251  
Db 132 LKLEELHLDNDSITGVGEDGAFREAIKLLFLSKNHLSSVPVGLPVDQLRLVDENR 191  
Qy 252 ISTVELEDFRYKELQRLGLGNKKTID--IENGSLANIPRVREIHLNKKIKPSGLPE 309  
Db 192 IAVSDMAFQNLTSERLIVDGNLLTNKGAEGTFSHLTKKEFSIYVNSLSHPPDPLG 251  
Qy 310 LKYLQIIFLHNSIARVGVNDPCPTVPKMKKSLYSALSIFNNPVK 354  
Db 252 THLIR-LYLODNQINHIPLTAF-SNLRKLER-----LDISNNQLR 289

RESULT 40  
US-09-904-011-28  
Sequence 28, Application US/09904011

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; Publication No. US20030003530A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,011
; PRIOR FILING DATE: 2001-07-11
; PRIOR FILING DATE: 2000-09-18
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; PRIOR FILING DATE: 2000-02-22
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; PRIOR APPLICATION NUMBER: US 60/145,698
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; PRIOR APPLICATION NUMBER: US 60/146,222
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; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 28
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo Sapien

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US-09-904-011-28

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Query Match      15.7%; Score 313.5; DB 9; Length 660;
Best Local Similarity 27.7%; Pred. No. 1.4e-18;
Matches 79; Conservative 62; Mismatches 109; Indels 35; Gaps 8;

QY 74 CPFGCOCYSRVVHCSDGLTSTVPTNIPFDTRMLDLQNNKIKEKENDFKGLTSLYGLILN 133
Db 36 CPVCRCDNFVYCNERSLTSPVLGIP-----EGVTVLY---LH 71
QY 134 NNKLTKI-HPKAEFLTTKLRLRYLSHNSQLSEIPLNLPKSLAEIRIHENKVKIKQDKTFKG 192
Db 72 NNQINNAGPPAELHNVSQVHTVLYGNDLDEPMMNLPKVVRVHLQENNIQIISRAALAQ 131
QY 193 MNALHVLMSANPLDNNGIEPGAF-EGVTVFHIRIAEAKLTSPKGLPPTLLEHLHDYKN 251
Db 132 LLKLEELHLDDNSISTVGVEDGAFREAIKLLFLSKNHLSSVPGVLDLQELRVDENR 191
QY 252 ISTVELEDFKRYKELQRLGIGNNKITD--IENGSLANIPRVREIHLNKKIKIPSGLPE 309
Db 192 IAVISDMATQNLTSLERLIVDGNLLTNKGLAEGTFSHLTKLKEFSIVRNSLSHPPDLP 251
QY 310 LKYLQIIFLHSNSIARVGVNDFCTVPKMKKSLYSALSIFNNPVK 354
Db 252 THLIR-LYLQDNQINHIPLTAF-SNLRKLER-----LDISNNQLR 289

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RESULT 41

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US-10-028-072-350
; Sequence 350, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028,072
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19

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;	PRIOR FILING DATE: 1998-03-25	
;	PRIOR APPLICATION NUMBER: 60/079663	
;	PRIOR FILING DATE: 1998-02-27	
;	PRIOR APPLICATION NUMBER: 60/079728	
;	PRIOR FILING DATE: 1998-03-27	
;	PRIOR APPLICATION NUMBER: 60/080165	
;	PRIOR FILING DATE: 1998-03-31	
;	PRIOR APPLICATION NUMBER: 60/081203	
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;	PRIOR APPLICATION NUMBER: 60/081229	
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;	PRIOR APPLICATION NUMBER: 60/081695	
;	PRIOR FILING DATE: 1998-04-14	
;	PRIOR APPLICATION NUMBER: 60/081817	
;	PRIOR FILING DATE: 1998-04-15	
;	PRIOR APPLICATION NUMBER: 60/081818	
;	PRIOR FILING DATE: 1998-04-15	
;	PRIOR APPLICATION NUMBER: 60/082999	
;	PRIOR FILING DATE: 1998-04-24	
;	PRIOR APPLICATION NUMBER: 60/083322	
;	PRIOR FILING DATE: 1998-04-28	
;	PRIOR APPLICATION NUMBER: 60/083545	
;	PRIOR FILING DATE: 1998-04-29	
;	PRIOR APPLICATION NUMBER: 60/084600	
;	PRIOR FILING DATE: 1998-05-07	
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;	PRIOR FILING DATE: 1998-05-07	
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;	PRIOR APPLICATION NUMBER: 60/085149	
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;	PRIOR APPLICATION NUMBER: 60/088730	
;	PRIOR FILING DATE: 1998-06-10	
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;	PRIOR FILING DATE: 1998-06-10	
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;	PRIOR FILING DATE: 1998-06-11	
;	PRIOR APPLICATION NUMBER: 60/089532	
;	PRIOR FILING DATE: 1998-06-17	
;	PRIOR APPLICATION NUMBER: 60/089599	
;	PRIOR FILING DATE: 1998-06-17	
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;	PRIOR APPLICATION NUMBER: 60/090429	
;	PRIOR FILING DATE: 1998-06-24	
;	PRIOR APPLICATION NUMBER: 60/090445	
;	PRIOR FILING DATE: 1998-06-24	

; PRIOR APPLICATION NUMBER: 60/090538  
 ; PRIOR FILING DATE: 1998-06-24  
 ; PRIOR APPLICATION NUMBER: 60/090863  
 ; PRIOR FILING DATE: 1998-06-26  
 ; PRIOR APPLICATION NUMBER: 60/091360  
 ; PRIOR FILING DATE: 1998-07-01  
 ; PRIOR APPLICATION NUMBER: 60/091519  
 ; PRIOR FILING DATE: 1998-07-02  
 ; PRIOR APPLICATION NUMBER: 60/091982  
 ; PRIOR FILING DATE: 1998-07-07

Query Match 15.7%; Score 313.5; DB 9; Length 660;  
 Best Local Similarity 27.7%; Pred. No. 1.4e-18;  
 Matches 79; Conservative 62; Mismatches 109; Indels 35; Gaps 8;

QY 74 CPFGCQCYRVVHCSDGLTSTVPTNIPEDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133  
 Db 36 CPVSCRCDRNFVYCNERSLTSPVLPGLP-----EGVTVLY---LH 71  
 QY 134 NNKLTKI-HPKAFLTTKRLRLYLHSHNOLSEIPLNPKSLAEIRIHENKVKIKQKDFKG 192  
 Db 72 NNQINNAGFAELHNVQSVHTVLYGNQDDEFFPMNLPKNRVVHLHQQENNIQTISRALAQ 131  
 QY 193 MNALHVLEMSANPLDNNNGIEGAF-EGVTVFHIRIAEAKLTSPKGLPPTLLEHLHDYKN 251  
 Db 132 LLKLEELHLDNDSISTVGVEDGAFREATISLKLFLSKNHLSSVPVGLPVDLQELRVDENR 191  
 QY 252 ISTVELEDFKRYKELQRLGLGNKTKD--IENGSLANTPRVREIHLNKKLKIPSGLPE 309  
 Db 192 IAVISDMAFQNTLSERLIVDGNLTNKGIAEGTFSHTTKUKFESIVRNSLSHPHPPDLPG 251  
 QY 310 LKYLQIIFLHNSIARVGVNDPCPTVPKMKKSLYSALSIFNNPVK 354  
 Db 252 THLIR-LYLOQNOINHPIPTAF-SNLRKLER-----LDISNNQLR 289

RESULT 42

US-09-909-320-28  
 ; Sequence 28, Application US/09909320  
 ; Patent No. US20020132240A1

GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, A.  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth, J.  
 ; APPLICANT: Klijavin, Ivar J.  
 ; APPLICANT: Mather, Jennie P.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William, I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: 10466-14  
 ; CURRENT APPLICATION NUMBER: US/09/909,320  
 ; CURRENT FILING DATE: 2002-01-04  
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414  
 ; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048  
 ; PRIOR FILING DATE: 1999-07-07  
 ; PRIOR APPLICATION NUMBER: US 60/145,698  
 ; PRIOR FILING DATE: 1999-07-26  
 ; PRIOR APPLICATION NUMBER: US 60/146,222  
 ; PRIOR FILING DATE: 1999-07-28  
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594  
 ; PRIOR FILING DATE: 1999-09-08  
 ; PRIOR APPLICATION NUMBER: PCT/US99/20944  
 ; PRIOR FILING DATE: 1999-09-13  
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090  
 ; PRIOR FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547  
 ; PRIOR FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: PCT/US99/23089  
 ; PRIOR FILING DATE: 1999-10-05  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28214  
 ; PRIOR FILING DATE: 1999-11-29  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313  
 ; PRIOR FILING DATE: 1999-11-30  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28564  
 ; PRIOR FILING DATE: 1999-12-02  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28565  
 ; PRIOR FILING DATE: 1999-12-02  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095  
 ; PRIOR FILING DATE: 1999-12-16  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30911  
 ; PRIOR FILING DATE: 1999-12-20  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30999  
 ; PRIOR FILING DATE: 1999-12-20  
 ; PRIOR APPLICATION NUMBER: PCT/US00/00219  
 ; PRIOR FILING DATE: 2000-01-05  
 ; NUMBER OF SEQ ID NOS: 423  
 ; SEQ ID NO 28  
 ; LENGTH: 660  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-909-320-28

Query Match

15.7%; Score 313.5; DB 10; Length 660;  
 Best Local Similarity 27.7%; Pred. No. 1.4e-18;  
 Matches 79; Conservative 62; Mismatches 109; Indels 35; Gaps 8;

QY 74 CPFGCQCYRVVHCSDGLTSTVPTNIPEDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133  
 Db 36 CPVSCRCDRNFVYCNERSLTSPVLPGLP-----EGVTVLY---LH 71  
 QY 134 NNKLTKI-HPKAFLTTKRLRLYLHSHNOLSEIPLNPKSLAEIRIHENKVKIKQKDFKG 192  
 Db 72 NNQINNAGFAELHNVQSVHTVLYGNQDDEFFPMNLPKNRVVHLHQQENNIQTISRALAQ 131  
 QY 193 MNALHVLEMSANPLDNNNGIEGAF-EGVTVFHIRIAEAKLTSPKGLPPTLLEHLHDYKN 251  
 Db 132 LLKLEELHLDNDSISTVGVEDGAFREATISLKLFLSKNHLSSVPVGLPVDLQELRVDENR 191  
 QY 252 ISTVELEDFKRYKELQRLGLGNKTKD--IENGSLANTPRVREIHLNKKLKIPSGLPE 309  
 Db 192 IAVISDMAFQNTLSERLIVDGNLTNKGIAEGTFSHTTKUKFESIVRNSLSHPHPPDLPG 251  
 QY 310 LKYLQIIFLHNSIARVGVNDPCPTVPKMKKSLYSALSIFNNPVK 354  
 Db 252 THLIR-LYLOQNOINHPIPTAF-SNLRKLER-----LDISNNQLR 289

RESULT 43

US-09-909-088B-28  
 ; Sequence 28, Application US/09909088B  
 ; Patent No. US20020146709A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Genentech, Inc.  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc







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; CURRENT APPLICATION NUMBER: US/10/175,737
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 290
; LENGTH: 1523
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-737-290

Query Match      15.5%; Score 309; DB 9; Length 1523;
Best Local Similarity 24.9%; Pred. No. 9.6e-18;
Matches 98; Conservative 58; Mismatches 114; Indels 124; Gaps 9;

Qy 74 CPFGCQSVRVHCSDLGLTSVPTNPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
Db 34 CPTKCTSAASVDCHGLGLRAVPRGIPRPAERLDLDRNNITRITKMDPAGLKNLRVLHLE 93
Qy 134 NNKLTKIHPKAFLLTKLRLRLYLSHNSLSEIPLNLPKS---LAEIRIHENKVKKIQKDTF 190
Db 94 DNQSVIERGAFQDLKQLERLRNKNKQLVLPPELLFQSTPKLTRLDLSENOIQIGIPKAF 153
Qy 191 KGMNALHVLMSANPLDNG---IEPGAPEG-----VTVP----- 222
Db 154 RGITDVKNLQ-----LDNNHISCIEDGAFRALRDLEILTLLNNNISRLVTSFNHMPKIR 208
Qy 223 -----HIR---IAEAK----- 230
Db 209 TLRHLSNHLCDCHLAWLSDWLRQRTVGOFTLCMAPVHLRGFNVADVQKKEYVCAPHS 268
Qy 231 -----LTSVPKGLPPTLLELHLHDYNNKISTVELEDFK 261
Db 269 EPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIVEIRLEQNSIKAIPAGFT 328
Qy 262 RYKELQRLGLGNKNTIDENGSLANIPRVREIHLNKKLKKIPSGLPE-LKYLIQIFLHS 320
Db 329 QYKCLKRIDISKNOISDIADPAFOGLKSLTSLVLYGNKITEIAKGLFDGLVSLQLLLLNA 388
Qy 321 NSIARVGVNDFCPTVPKMKKSLYSASISLNNPVK 354
Db 389 NKINCLRVNTF-----QDLQNLNLSLYDNKLQ 416

RESULT 49
US-10-052-586-290
; Sequence 290, Application US/10052586
; Patent No. US20020127584A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/052,586
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063564
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063734
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063870
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/064103

Query Match      15.5%; Score 309; DB 12; Length 1523;
Best Local Similarity 24.9%; Pred. No. 9.6e-18;
Matches 98; Conservative 58; Mismatches 114; Indels 124; Gaps 9;

Qy 74 CPFGCQSVRVHCSDLGLTSVPTNPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
Db 34 CPTKCTSAASVDCHGLGLRAVPRGIPRPAERLDLDRNNITRITKMDPAGLKNLRVLHLE 93
Qy 134 NNKLTKIHPKAFLLTKLRLRLYLSHNSLSEIPLNLPKS---LAEIRIHENKVKKIQKDTF 190
Db 94 DNQSVIERGAFQDLKQLERLRNKNKQLVLPPELLFQSTPKLTRLDLSENOIQIGIPKAF 153
Qy 191 KGMNALHVLMSANPLDNG---IEPGAPEG-----VTVP----- 222
Db 154 RGITDVKNLQ-----LDNNHISCIEDGAFRALRDLEILTLLNNNISRLVTSFNHMPKIR 208
Qy 223 -----HIR---IAEAK----- 230
Db 209 TLRHLSNHLCDCHLAWLSDWLRQRTVGOFTLCMAPVHLRGFNVADVQKKEYVCAPHS 268
Qy 231 -----LTSVPKGLPPTLLELHLHDYNNKISTVELEDFK 261
Db 269 EPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIVEIRLEQNSIKAIPAGFT 328
Qy 262 RYKELQRLGLGNKNTIDENGSLANIPRVREIHLNKKLKKIPSGLPE-LKYLIQIFLHS 320
Db 329 QYKCLKRIDISKNOISDIADPAFOGLKSLTSLVLYGNKITEIAKGLFDGLVSLQLLLLNA 388
Qy 321 NSIARVGVNDFCPTVPKMKKSLYSASISLNNPVK 354
Db 389 NKINCLRVNTF-----QDLQNLNLSLYDNKLQ 416

RESULT 48
US-10-011-064-2
; Sequence 2, Application US/10011064
; Patent No. US20020123104A1
; GENERAL INFORMATION:
; APPLICANT: Connolly, Timothy
; APPLICANT: Rajput, Bhanu
; TITLE OF INVENTION: Human Slit Polypeptide and Polynucleotides Encoding
; TITLE OF INVENTION: Same
; FILE REFERENCE: 640100-443
; CURRENT APPLICATION NUMBER: US/10/011,064
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/063,946
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/096,420
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1523
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-011-064-2

Query Match      15.5%; Score 309; DB 12; Length 1523;
Best Local Similarity 24.9%; Pred. No. 9.6e-18;
Matches 98; Conservative 58; Mismatches 114; Indels 124; Gaps 9;

Qy 74 CPFGCQSVRVHCSDLGLTSVPTNPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
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[illegible]

; PRIOR FILING DATE: 1998-06-16  
 ; PRIOR APPLICATION NUMBER: 60/089514  
 ; PRIOR FILING DATE: 1998-06-16  
 ; PRIOR APPLICATION NUMBER: 60/089538  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: 60/089598  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: 60/089653  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: 60/089908

Query Match 15.5%; Score 309; DB 12; Length 1523;  
 Best Local Similarity 24.9%; Pred. No. 9.6e-18;  
 Matches 98; Conservative 58; Mismatches 114; Indels 124; Gaps 9;

Qy	74	CPFGCQCYSRVHCHSDGLTSTPTNIPEDTRMLDQNNKKEIKENDFKGLTSLYGLILN	133
Db	34	CPTKCTSAASVCHGLRAVRPGIPRPAERLDLDNRNTRITKMDFAGLKRLRVLHLE	93
Qy	134	NNKTKIHPKAFLLTKRLRYLSHNSLSEIPLNPKS----LAELRIHENKVKKIQKDTF	190
Db	94	DNQSVIERGAFQDKLERLRLKNNKQLVLPPELLFQSTPKLTRLDSLSENQIQGIPKAF	153
Qy	191	KCMNALHVLEMSANPLDNG---IEPCAFEG-----VTVP-----	222
Db	154	RGITDVRNLQ-----LDNNHTISCIEDGAFRALRDLEILTLLNNNNISRLVTSFNHMPKIR	208
Qy	223	-----HIR---IAEAK-----	230
Db	209	TLRLSHNYLCHLAWLSDWLRQRTVQGTLCMAVHLRGFNADVQKKEYVCAPHS	268
Qy	231	-----TSPVKGLPPTLLEHLHDYNNKISTVELEDFK	261
Db	269	EPPSCNANSISCPSPCTCSNNIVDCRGKGLMETPANLPEGIVEIRLEQNSIKAIPAGFT	328
Qy	262	RYKELQRLGLGNKNTIDENGSLANIPRVREIHLNENKLLKIPSGLPE-LKYLIQLFLHS	320
Db	329	QYKRLRIDISKNGISDIADPAFOGLKSLTSLVLYGNKITEIAKAGLFDGLVSLQULLLNA	388
Qy	321	NSIARVGVNDPCTVPVKMKKSLXSALSIFNNPVK	354
Db	389	NKINCLRVNTF-----QDLQNLNLLSLYDNKLQ	416

RESULT 50

US-10-063-547-124  
 ; Sequence 124, Application US/10063547  
 ; Publication No. US20020182638A1

GENERAL INFORMATION:

; APPLICANT: Eaton, Dan J.  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3230R1C1  
 ; CURRENT APPLICATION NUMBER: US/10/063,547  
 ; CURRENT FILING DATE: 2002-05-02  
 ; Prior Application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 170  
 ; SEQ ID NO 124  
 ; LENGTH: 513  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien

Query Match 15.3%; Score 304.5; DB 9; Length 513;  
 Best Local Similarity 28.8%; Pred. No. 5.5e-18;

Matches	87;	Conservative	57;	Mismatches	105;	Indels	53;	Gaps	9;
Qy	74	CPFGCQCYSRVHCHSDGLTSTPTNIPEDTRMLDQNNKKEIKENDFKGLTSLYGLILN	133						
Db	34	CPFGCCECKWYVYCESQKLOEIPSSISACCLGLSLRYNSLOKLYNQFKGLNQLTWLYLD	93						
Qy	134	NNKTKIHPKAFLLTKRLRYLSHNSLSEIPLNPKSLAELRIHENKVKKIQKDTFKGM	193						
Db	94	NNHISNIDENAFNGIRRLKELILSSNRISYF-LN-----NTERPV	132						
Qy	194	NALHVLEMSANPLDNGIEPCAFEGVTVFHTRIAEAKLTSVPKGLPPTLLEHLHDYNNKIS	253						
Db	133	TMLRNLDSLYNOLHSLGSE--QFRGLR-----KLLSLHURSNLSR	170						
Qy	254	TVELEDFKRYKELQRLGLGNKNTIDENGSLANIPRVREIHLNENKLLKIPSGL-PELKY	312						
Db	171	TIPVRIFQDCRNLELLDLGYNRIRSLARNVFAGMIRLKLHLEHNFQSKLNLALFPRLVS	230						
Qy	313	LQIIFLHNSIARVGVNDPCTVPVKMKKSLXSALSIFNNPVKYMEMPATFCV--LSRM	370						
Db	231	LQNLVLYQNNKISVIG-----QTMSTWSSSL-ORLDSLGNTEAFS-GPSVFQCVNQLRL	283						
Qy	371	SV	372						
Db	284	NL	285						

Search completed: January 24, 2003, 12:30:51  
 Job time : 19 secs

Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	1040.5	52.2	369	2	S32793	biglycan precursor
2	1037.5	52.1	369	2	S20811	proteoglycan I - m
3	1034	51.9	368	1	BGHUN	biglycan precursor
4	1024.5	51.4	369	2	S32559	biglycan precursor
5	969	48.6	357	2	S24317	decorin precursor
6	963.5	48.4	359	1	NBHUC8	decorin precursor
7	943	47.3	360	2	S06280	decorin precursor
8	941	47.2	360	2	I47020	decorin - rabbit
9	907.5	45.6	354	2	A35434	decorin precursor
10	899	45.1	354	2	S29145	decorin precursor
11	399.5	20.1	343	2	A41748	lumican precursor
12	384	19.3	342	2	A46743	lumican precursor
13	378	19.0	338	2	S52284	lumicon, secretory
14	358.5	18.0	382	2	I39068	proline- arginine-
15	342.5	17.2	375	2	S05390	fibromodulin precu
16	333.5	16.7	380	2	S17876	fibromodulin - chi
17	324	16.3	1523	2	T13953	MEGF5 protein - ra
18	323	16.2	1531	2	T42218	slit-1 protein hom
19	318	16.0	376	2	S55275	fibromodulin precu
20	316	15.9	1469	2	B36665	slit protein 2 pre
21	316	15.9	1480	2	A36665	slit protein 1 pre
22	296	14.9	1091	2	A35852	glial cell membran
23	294	14.8	361	2	A53860	chondroadherin pre
24	282.5	14.2	1025	2	T42626	secreted leucine-r
25	272	13.7	603	2	JC1282	insulin-like growt
26	266	13.4	707	2	JC7763	neuronal leucine-r
27	265	13.3	603	2	JC6128	insulin-like growt
28	265	13.3	1051	2	T13174	gp150 protein - fr
29	261.5	13.1	907	2	JG0193	G protein-coupled

—

[illegible]

A:Residues: 301-308  
A:Cross-references: EMBL:U11686; NID:g607862; PIDN:AAC50117.1; PID:g619606  
R:Fishel, L.W.; Termino, J.D.; Young, M.F.  
J. Biol. Chem. 264, 4571-4576, 1989  
A:Title: Deduced protein sequence of bone small proteoglycan I (Biglycan)  
A:Reference number: A32458; MUID:89174714; PMID:2647739  
A:Accession: A32458  
A:Molecule type: mRNA  
A:Residues: 1-138, 'NV', 141-162, 'DV', 165-368 <FIS2>  
A:Cross-references: GB:J04593; NID:g184339  
A:Note: parts of this sequence, including the amino end of the mature protein, are identical to the deduced sequence of the mature protein.  
A:Note: the translated sequence in GenBank entry HUMHFGI, release 113.0, is identical to the deduced sequence.  
R:Stoecker, G.; Meyer, H.F.; Wagener, C.; Greiling, H.  
Biochem. J. 274, 415-420, 1991  
A:Title: Purification and N-terminal amino acid sequence of a chondroitin sulfate proteoglycan from bovine nasal septum



F;231-254/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
F;255-278/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
F;279-301/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
F;302-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LRP>  
F;317-369/Domain: proteoglycan carboxyl-terminal homology <PCH>  
F;42,48/Binding site: dermatan sulfate (Ser) (covalent) #status experimental  
F;181,199/Binding site: dermatan sulfate (Ser) (covalent) #status predicted  
F;271,312/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match            51.4%   Score 1024.5; DB 2; Length 369;  
Best Local Similarity   52.1%; Prod. No. 1.5e-62;  
Matches 196; Conservative 65; Mismatches 96; Indels 19; Gaps 3;

QY      6 LLLFLALCSAKPPSPSHIALKNMMLKDMEDTDDDDD-----D DDDDDDEDNSLFPTREP 61  
       | ||| |||| | | | | : | : |  
DB      7 LAALLASQUALPFEPQ-----KAFWDFTLDDGGLPMLNDEEASAETTSIGIPDLDS 55  
       | ||| |||| | | | | : | : |  
QY      62 RSHFFFPDLPMPCFGQCYSRVVHCSDLGITSVTPNIFPDTRMDLQNKKIKRIKENDF 121  
       | ||| |||| | | | | : | : |  
DB      56 ----LPPTYSAMCFPGCGHLVRVQCSDLGLKAVPKESIDPTLTLLDQLONNDISELRKDGF 111  
       | ||| |||| | | | | : | : |  
QY      122 KGLTSLYLGINNNKLTKIHPKAPLTATKYRLRYLSHNLSEPLNPILSKSLAEURIHENK 181  
       | ||| |||| | | | | : | : |  
DB      112 KGLOHLXALVLNVNKISKIEKAFSPURKLUKLYISKHVLVEIPPNPSSLVLELIHRDNR 171  
       | ||| |||| | | | | : | : |  
QY      182 VKTIKTDTFKGMNALHVLEMSANPLDNNGTEPGAFAEGVTVFHIRIAEAKTIVPVKGLPPT 241  
       | ||| |||| | | | | : | : |  
DB      172 IRKPVGVSGLRNMCIMMGPNLENSEPGEPAFDGLKLYLRISAELTGIPKDLPET 231  
       | ||| |||| | | | | : | : |  
QY      242 LLEUHDYNKISTVEDEFKRYPELQRGLGNKKITDIENSGLANIPRVREIHLENNKLK 301  
       | ||| |||| | | | | : | : |  
DB      232 LNELUDHNKIQTAELEDLARLYSRKLYRGIGHGNIRMIENGSLFSFLTRELHLDNNKLS 291  
       | ||| |||| | | | | : | : |  
QY      302 KIPSGLPELAYLOTIELHSNISARGVNDRCPTVPKMKSILSAISLFNPNVKYWEMOQA 361  
       | ||| |||| | | | | : | : |  
DB      292 RVPAGLFDLKLQQVVYLHTNNITYKVGVNDRCVPGCFGWKRAYNYGISLFNPNVPWWEVOA 351  
       | ||| |||| | | | | : | : |  
QY      362 TFCVLSRMVSVOLGNF 377  
       | ||| |||| | | | | : | : |  
DB      352 TFRCVTDRLAIQFNQY 367  
       | ||| |||| | | | | : | : |

RESULT 5  
S24317  
decorin precursor - chicken  
N:Alternate names: corneal chondroitin/dermatan sulfate proteoglycan  
C:Species: Gallus gallus (chicken)  
C>Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text\_change 20-Aug-1999  
C:Accession: S24317; S58474; S22197  
R:Lil, W.; Vergnes, J.P.; Cornuet, P.K.; Hassell, J.R.  
Arch. Biochem. Biophys. 296, 190-197, 1992  
A>Title: cDNA clone to chick corneal chondroitin/dermatan sulfate proteoglycan reveals F;1-16/Domain: signal sequence #status predicted <SIG>  
F;17-30/Domain: propeptide #status predicted <PRO>  
F;31-357/Product: decorin #status experimental <MAT>  
F;46-70/Domain: proteoglycan amino-terminal homology <PAH>  
F;80-103/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
F;104-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F;128-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F;149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
F;173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
F;199-219/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
F;220-243/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
A:Reference number: S24317; PMID:92296755; PMID:1605630  
A:Accession: S24317  
A:Molecule type: mRNA  
A:Residues: 1-357 <LIA>  
A:Cross-references: EMBL:X63797; NID:g62887; PIDN:CAA45318.1; PTD:g62888  
A:Accession: S58474  
A:Molecule type: protein  
A:Residues: 31-33,'X','35'-39,'X','41-48,'X','50-51 <LIA>  
C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan C:Keywords: collagen binding; extracellular matrix; glycoprotein  
F;1-16/Domain: signal sequence #status predicted <SIG>  
F;17-30/Domain: propeptide #status predicted <PRO>  
F;31-357/Product: decorin #status experimental <MAT>  
F;46-70/Domain: proteoglycan amino-terminal homology <PAH>  
F;80-103/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
F;104-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F;128-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F;149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
F;173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
F;199-219/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
F;220-243/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>

RESULT 5  
S24317  
decorin precursor - chicken  
N:Alternate names: corneal chondroitin/dermatan sulfate proteoglycan  
C:Species: Gallus gallus (chicken)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Aug-1999  
C:Accession: S24317; S58474; S22197  
R:Li, W.; Vergnes, J.P.; Cornuet, P.K.; Hassell, J.R.  
Arch. Biochem. Biophys. 296, 190-197, 1992  
A:Title: cDNA clone to chick corneal chondroitin/dermatan sulfate proteoglycan reveals  
A:Reference number: S24317; MUID:92296755; PMID:1605630  
A:Accession: S24317  
A:Molecule type: mRNA  
A:Residues: 1-357 <LIW>  
A:Cross-references: EMBL:X63797; NID:G62887; PIDN:CAA45318.1; PID:G62888  
A:Accession: S58474  
A:Molecule type: protein  
A:Residues: 31-33,'X',35-39,'X',41-48,'X',50-51 <LIA>  
C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan  
C:Keywords: collagen binding; extracellular matrix; glycoprotein  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:17-30/Domain: propeptide #status predicted <PRO>  
F:31-357/Product: decorin #status experimental <MAT>  
F:46-70/Domain: proteoglycan amino-terminal homology <PAH>  
F:80-103/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
F:104-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
F:128-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F:149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F:173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
F:199-219/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
F:220-243/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>

F;244-267/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>  
F;268-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>  
F;291-305/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical  
F;306-357/Domain: proteoglycan carboxyl-terminal homology <PC>

	Query Match	48.6%; Score 969; DB 2; Length 357;
	Best Local Similarity	50.0%; Pred. No. 8.9e-59;
Matches	187; Conservative	65; Mismatches 98; Indels 24; Gaps 4;

QY 5 VLLLFALCSAKFFSPSHIALKNMKMEDPTDDDDDDDDDDDEDNSLFPTRPRSH 64  
      :| |: | :| | :| | :| | :| | :| | :| | :| | :| | :  
Db 6 LFVLLLPVCILATRFHQK--GLDFDEIEDGSAD-----MAPTDDPVIS 46  
  
QY 65 FPFEDLPPMPFCQCYSRVVVHSCDILGTSVTNPIDFTRMLDLQNKKTEIKENDFKGL 124  
      | :| | | | | | | | | | | | | | | :| | :| | | | | | | | | |  
Db 47 GFP----PVPFCQCHRLVRVQSDIGLERPKDLDPDTLLDLQNNKITELKEGDFKL 102  
  
QY 125 TSLYGILLNKKITKHIPKAFLTTKRLRLYLTHSNHLSEIPLMLPSLAELRIHENKVKK 184  
      :| |: | | | | | | | | | | | | | | :| | | | | | | | | | |  
Db 103 KNLHALILVNKISKISPAFAFLKLELYLSKNNLKELPENMPSQLQEIRAHENEISK 162  
  
QY 185 IQKDTFKGMNALHVLEMSANPLDNNGIEPGAFGV-TVPHIRIAEAKLVSVKGLIPTTL 243  
      :|| | | | | | | | | | | | | | | | :| | | | | | | | | | |  
Db 163 LRRAVFNLGNVLIVBELGTNPKSSGIENGAFOCMKRLSYIRTADTNITSIPKGLPPSUT 222  
  
QY 244 ELHDYNKISTVELEDKFVKYEQRGLGNGNKTTDIENGSLANIPRVREIHLENKKIKKI 303  
      || | | | | | | | | | | | | | | | :| | | | | | | | | | |  
Db 223 ELLHDGNKISKIDAEGLSGLTLNAKLGLSFNSSISSVENGLNVPHLRHLNNNELVRV 282  
  
QY 304 PSGLPELKYLIQTILHSNSTARVGVDNFDCTVPKMKKSLYSAISLNPNPVKWEMOPATF 363  
      |||| | | | | | | | | | | | | | | | || | | | | | | | | | |  
Db 283 PSGLGEHKYTQVYLYHNKKIASIGINDFCLGYNTKKATYSGVSFSNPVQWEIQPSAF 342  
  
QY 364 RCVLSRMSVOLGNF 377  
      || | | | | | | |  
Db 343 RCTHERSAVOIGNY 356  
      | | | | | | | |

RESULT 6  
NBHUC8  
N:Alternate names: cartilage proteoglycan protein II; DS-PG II; PG40 core protein; p;r  
C:Species: Homo sapiens (man)  
C>Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 21-Jan-2000  
C:Accession: A45016; B45015; A26476; S05640  
R:Vetter, U.; Vogel, W.; Just, W.; Young, N.F.; Fisher, L.W.  
Genomics 15, 161-168, 1993  
A:Title: Human decorin gene: intron-exon junctions and chromosomal localization.  
A:Reference number: A45016; UID:93162643; PMID:8432527  
A:Accession: A45016  
A:Molecule type: DNA  
A:Residues: 1-359 <YET>  
A:Cross-references: GB:L01125; GB:L01126; GB:L01127; GB:L01128; GB:L01129; GB:L01130;  
A>Note: sequence extracted from NCBI backbone (NCBIP:125061)  
R:Danielson, K.G.; Fazizlo, A.; Cohen, I.; Cannizzaro, L.A.; Eichstetter, I.; Iozzo, R.  
Genomics 35, 146-160, 1993  
A:Title: The human decorin gene: intron-exon organization, discovery of two alternati  
A:Reference number: A45015; UID:93162642; PMID:8432526  
A:Accession: A45015  
A>Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 28-70 <DA2>  
A:Cross-references: GB:M98262  
A>Note: sequence extracted from NCBI backbone (NCBIP:125013)  
A:Accession: B45015  
A>Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 296-359 <DNA>  
A>Note: sequence extracted from NCBI backbone (NCBIP:125017)  
R:Kräusius, T.; Ruoslahti, E.  
Proc. Natl. Acad. Sci. U.S.A. 83, 7683-7687, 1986  
A:Title: Primary structure of an extracellular matrix proteoglycan core protein deduc  
A:Reference number: A26476; UID:87017013; PMID:3484330



A:Accession: A26476  
A:Molecule type: mRNA  
A:Residues: 1-359 <KRU>  
A:Cross-references: GB:M14219; NID:g181169; PIDN:AAB00774.1; PID:g181170  
R:Noughley, P.J.; White, R.J.  
Biochem. J. 262, 823-827, 1989  
A:Title: Dermatan sulphate proteoglycans of human articular cartilage. The properties of  
A:Reference number: S05639; MUID:90073579; PMID:2590169  
A:Accession: S05640  
A:Molecule type: protein  
A:Residues: 31-33, X, 35-50 <R0U>  
C:Comment: This protein binds type I collagen.  
C:Genetics:  
A:Gene: GDB:DCN  
A:Cross-references: GDB:119839; OMIM:125255  
A:Map position: 12q21.3-12q23  
A:Introns: 71/1; 108/3; 180/1; 218/1; 249/2; 295/3  
A>Note: The first two introns occur before the initiator codon  
C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan  
C:Keywords: chondroitin sulfate proteoglycan; collagen binding; dermatan sulfate, dupli  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:17-30/Domain: propeptide #status predicted <PRO>  
F:31-359/Product: decorin #status predicted <MPT>  
F:48-72/Domain: proteoglycan amino-terminal homology <PAH>  
F:82-105/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
F:106-125/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
F:130-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F:151-174/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F:175-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
F:201-221/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
F:222-245/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
F:246-269/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
F:270-292/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
F:293-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>  
F:308-359/Domain: proteoglycan carboxyl-terminal homology <PRC>  
F:34/Binding site: dermatan sulfate (Ser) (covalent) #status experimental  
F:189,325/Binding site: dermatan sulfate (Ser) (covalent) #status predicted  
F:211,262,303/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 48.4%; Score 963.5; DB 1; Length 359;  
Best Local Similarity 50.4%; Pred. No. 2.1e-58;  
Matches 191; Conservative 65; Mismatches 100; Indels 23; Gaps 4;  
QY 1 MKEYVLLFLALCS-AKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFPTR 59  
Db 1 MKATIIILLLAQVSWAGPF---QQQGLDFMLEDASGIGVEPDDR-----45  
QY 60 EPRSHFFPDLFPMCPFCQCYSRVVHSCDGLTSVPTNPFDTMLDLQNNKIKEIKEN 119  
Db 46 -----FEPSPGVPFCQCHLRVQCSGLGLDKVPKDLPPDPTLLDLQNNKIKEIKG 99  
QY 120 DFKGLTSYGLILNNKLTIKHPKAFLLTKLRRLYLSHNOLSEIPLNPKSLAEIRHE 179  
Db 100 DFKNLKHALILVNNKISKVSGAFTPLVKLERLYLSKNOLKELPKMKPTQLQELRAHE 159  
QY 180 NKVKIKQIDTFKGMNALHVLMSANPLDNNNGIEPGAFGV-TVPHIRIATAKLTSPVKGL 238  
Db 160 NEITKVRKVTENGLOMIVIELGTNPLKSSGICNGAQQMKKLYIRIADTNITSIQGL 219  
QY 239 PPTLEHLHDYKISTVELEDFEKYKELQRLGLGNKKITDIENGLANIPRVRIHLNEN 298  
Db 220 PPSUTELHLDGKNSRVDAAALSKGLNNLAKGLSFSNSTSAVDNGSLANTPHLRHLHDNN 279  
QY 299 KKKTPSPGLPELKYLIQIFLHNSIARVGVNDFCTVPKMKSLYSATLSFNNPVKWEK 358  
Db 280 KLRVPGGLAEHKYIQVYLLHNNISVVGSSDFCPGHNTHKKASYSGVLSFNSNPVQWEI 339  
QY 359 QPATFRCVLSRMSVOLGNF 377  
Db 340 QPSTFRCVVRSALQNGY 358

Query Match 47.3%; Score 943; DB 2; Length 360;  
Best Local Similarity 49.1%; Pred. No. 5.3e-57;  
Matches 186; Conservative 69; Mismatches 102; Indels 22; Gaps 5;  
QY 1 MKEYVLLFLALCS-AKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDNSLFPTR 59  
Db 1 MKATIIILLLAQVSWAGPF---QQQGLDFMLEDASGIGVEPDDR-----45

S06280

decorin precursor - bovine  
N:Alternate names: dermatan sulfate proteoglycan II; proteoglycan core protein II  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 31-Mar-1990 #sequence.revision 31-Mar-1990 #text\_change 20-Aug-1999  
C:Accession: S06280; B31430; A26545; A20935  
R:Day, A.A.; McQuillan, C.I.; Termini, J.D.; Young, M.R.  
Biochem. J. 248, 801-805, 1987  
A:Title: Molecular cloning and sequence analysis of the cDNA for small proteoglycan I  
A:Reference number: S06280; MUID:88133946; PMID:3435485  
A:Accession: S06280  
A:Molecule type: mRNA  
A:Residues: 1-360 <DAY>  
A:Cross-references: EMBL:Y00712; NID:g618; PIDN:CAA68702.1; PID:g619  
A:Experimental source: bone  
R:Choi, H.U.; Johnson, T.L.; Pal, S.; Tang, L.H.; Rosenberg, L.; Neame, P.J.  
J. Biol. Chem. 264, 2876-2884, 1989  
A:Title: Characterization of the dermatan sulfate proteoglycans, DS-PGI and DS-PGII,  
A:Reference number: A31430; MUID:89123388; PMID:2914936  
A:Accession: B31430  
A:Molecule type: protein  
A:Residues: 31-33, X, 35-54 <CHO>  
A:Experimental source: cartilage; fetal skin  
R:Coster, L.; Rosenberg, L.C.; van der Rest, M.; Poole, A.R.  
J. Biol. Chem. 262, 3809-3812, 1987  
A:Title: The dermatan sulfate proteoglycans of bovine sclera and their relationship t  
A:Reference number: A26545; MUID:87137687; PMID:3818667  
A:Accession: A26545  
A:Molecule type: protein  
A:Residues: 31-50 <COS>  
A:Experimental source: sclera  
R:Pearson, C.H.; Winterbottom, N.; Fackre, D.S.; Scott, P.G.; Carpenter, M.R.  
J. Biol. Chem. 258, 15101-15104, 1983  
A:Reference number: A20935; MUID:84087911; PMID:6654908  
A:Accession: A20935  
A:Molecule type: protein  
A:Residues: 31-54 <PEA>  
A:Experimental source: skin  
R:Chopra, R.K.; Pearson, C.H.; Pringle, G.A.; Fackre, D.S.; Scott, P.G.  
Biochem. J. 232, 277-279, 1985  
A:Title: Dermatan sulphate is located on serine-4 of bovine skin proteodermatan sulph  
nces around glycosylation sites in different proteoglycans.  
A:Reference number: A44700; MUID:86103195; PMID:3936484  
A:Contents: annotation; glycosylation  
C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglyc  
C:Keywords: chondroitin sulfate proteoglycan; collagen binding; dermatan sulfate; ext  
F:1-15/Domain: signal sequence #status predicted <SIG>  
F:16-30/Domain: propeptide #status predicted <PRO>  
F:31-360/Product: decorin #status predicted <MAT>  
F:49-73/Domain: proteoglycan amino-terminal homology <PAH>  
F:83-106/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
F:107-130/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
F:131-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F:152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F:176-199/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
F:202-222/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
F:223-246/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
F:247-270/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
F:271-293/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
F:294-308/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>  
F:309-360/Domain: proteoglycan carboxyl-terminal homology <PCH>  
F:34/Binding site: dermatan sulfate (Ser) (covalent) #status experimental  
F:190,326/Binding site: dermatan sulfate (Ser) (covalent) #status predicted  
F:212,263,304/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 47.3%; Score 943; DB 2; Length 360;

Best Local Similarity 49.1%; Pred. No. 5.3e-57;

Matches 186; Conservative 69; Mismatches 102; Indels 22; Gaps 5;

QY 1 MKEYVLLFLALCS-AKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDNSLFPTR 59

Db 1 MKATIIILLLAQVSWAGPF---QQQGLDFMLEDASGIGVEPDDR-----45

RESULT 7





Qy	69	DLFPMCFPGQC---	YSRVVHCSDLGLTSVPTNIPFDTRMLDQNKKIKEIKENDEKFLT	125
		: ::  :	: ::  :	:
Db	32	ELSPCAPECNCPSHYPTAMYCDDLKLSVPM-VPGIKYILRNQIDHIDEKAENVTV	90	
Qy	126	SLYGLIINNKL--TKTHPKAFUTTTKKRLRYLISHNLSEIPNLNPKSLAEIRIHENKYK	183	
		: ::  :	: ::  :	:
Db	91	DLOWLIIDHNLLNSKITKGVSFKLQKLKHINYNMNTESVGPLPKSLQDLQLANNKIS	150	
Qy	184	KIQDITFGMNALHVLEMSANPLDNNGIEPCAFEGV-TVFHIRIAEAKLTSPVKGLPPTL	242	
		: ::  :	: ::  :	:
Db	151	KL--GSDGVGNVTTFIYLOHNQKEAVS-ASLKGLKSLEYLDLSFNQMSKLPAGLPTSU	207	
Qy	243	LEHLDDNKISTVELEDFKRYKELQRLGLGNKTIIDI-ENGSLANTPVREITHLENKKL	301	
		: ::  :	: ::  :	:
Db	208	LTYLDNNKTIINTPEYFNEFTGLQYLRLSHNELADSGVPGSNFISSLELDLSYNKKL	267	
Qy	302	KIPSGLPCLK-YLQIIIFLHSNSIARVGNVDFCTPYPMKKKSIYSAISLFFNPVKYWEMO	359	
		: ::  :	: ::  :	:
Db	268	SIPTVNENLENYLEV-----NKLEXFDVKSFCCKILGPLSYSKIHKLRDGNPLTQSLSL	322	
Qy	360	PATPRCV	366	
		:: :		
Db	323	PDMYECL	329	
		:: :		
		RESULT 14		
		I39068		
		proline-arginine-rich end leucine-rich repeat protein PRELP precursor - hu		
		C:Species: Homo sapiens (man)		
		C>Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 24-Sep-1999		
		C:Accession: I39068		
		R:Bengtsson, E.; Neame, P.J.; Heinegard, D.; Sommarin, Y.		
		J. Biol. Chem. 270, 25639-25644, 1995		
		A:Title: The primary structure of a basic leucine-rich repeat protein, PRELP		
		A:Reference number: I39068; MUID:96029653; PMID:7592739		
		A:Accession: I39068		
		A>Status: preliminary		
		A:Molecule type: mRNA		
		A:Residues: 1-382 <RES>		
		A:Cross-references: EMBL:U29089; NID:g886135; PIDN:AAC50230.1; PID:g886136		
		C:Genetics:		
		A:Gene: GDB:PRELP		
		A:Cross-references: GDB:696218		
		A:Map position: lq32.1-lq32.1		
		C:Superfamily: fibromodulin; leucine-rich alpha-2-glycoprotein repeat homo		
		C:Keywords: tandem repeat		
		Query Match 18.0%; Score 358.5; DB 2; Length 382;		
		Best Local Similarity 30.7%; Pred No. 4e-17;		
		Matches 90; Conservative 55; Mismatches 133; Indels 15; Gaps		
Qy	47	DDDEDNSLFPPTREPSSHFFPPDLFPMCFCGC---YSRVVHCSDLGLTSVPTNIPFD	103	
		: ::  :	: ::  :	:
Db	50	DEAPETDLPPLPPG---PPSIFPDCPRECVCPPDPFSALYCDSRNLKRPVP-IPPRI	104	
		: ::  :	: ::  :	:
Qy	104	RMLDQNNKIKEKENDPFKGLTSYGLIINNKLPIHKPAFLTWTKLRLLYLSNQISE	163	
		: ::  :	: ::  :	:
Db	105	HYYLYQNNFITELPVSFQNFATGLRWINDNRRIKDQRVLEKLPGLVFVIYMEKNQLEE	164	
		: ::  :	: ::  :	:
Qy	164	IPNLNPKSLAEIRIHENKYKTKQDKFGMNALHVLEMSANPLDNNGTEPGAFCGV-TVF	222	
		: ::  :	: ::  :	:
Db	165	VPSALPNLEQLRSLONSHISRTPPGVFSKLENLLDLLQHNRLSGVKPKDTFHGLKNIM	224	
		: ::  :	: ::  :	:
Qy	223	HIRIAEAKLTSPVKGLPPTLLEHLHDYINKISTVELEDFKRYKELQRLGLGNKTIIDI	280	
		: ::  :	: ::  :	:
Db	225	QLNALHNLKMPRPVPTAIHQYLDNSNIETIPNGCYKSPFNLAFLRLYNKLTDRGLP	284	
		: ::  :	: ::  :	:
Qy	281	NCSLANIPRVRETHLENKKLKTSPGLPELKYQIIIFLHSNSIARVGNVDFCP	333	
		: ::  :	: ::  :	:
Db	285	KNSF-NISNLLVLVLSHNRISSPAINRRLEHL---YLNNSIEIKHTQTICP	333	
		: ::  :	: ::  :	:



QY 223 -----HIR---IAEAK----- 230  
 Db 209 TLRHSNHYCDCHLAWLSDWLRQRTTIGQFTLCMAPVHLRGFSVADVQKKEYVCYPGPHS 268  
 QY 231 -----LTSVPKGLPPTLLEHLHDYNKISTVELEDEK 261  
 Db 269 EAPACNANSLSPACSCSNIVDCRGKGLUFEIPANIPGEIVIRLEQNSIKSIPAGAFI 328  
 QY 262 RYKELQRLGLGNKIIDTIENGSLANIPRVREIHLNENKAKIPSGLPE-LKYIQIIFLHS 320  
 Db 329 QYKCLKRIDISKNQISDIADPAFOGLKSLTSLVLYGNKITEIPKGLFDGLVSLQULLLNA 388  
 QY 321 NSIARVGVNDPCPTVPKMKKSLYSALSIFNNPVK 354  
 Db 389 NKINCLRVNTE-----QDLQNLNLLSLYDNKIQ 416  
 RESULT 18  
 T42218  
 slit-1 protein homolog - rat  
 N:Alternate names: MEGF4 protein  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 16-Aug-2002  
 C:Accession: T42218  
 R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.  
 Genomics 51, 27-34, 1998  
 A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs  
 A:Reference number: 214126; MUID:98360089; PMID:9693030  
 A:Accession: T42218  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1531 <NAK>  
 A:Cross-references: EMBL:AB011530; NID:g3449289; PIDN:BAA32460.1; PID:g3449290  
 A:Experimental source: strain Sprague-Dawley; brain  
 C:Genetics:  
 A:Gene: MEGF4  
 C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein

Query Match 16.28; Score 323; DB 2; Length 1531;  
 Best Local Similarity 25.08; Pred. No. 6.4e-14;  
 Matches 98; Conservative 64; Mismatches 116; Indels 114; Gaps 10;

QY 74 CPFGCQSVRVVHCSDLGTSVPTNIPFDT-----RMDL 108  
 Db 282 CPAMCSCSNGIVDCRGKGLTAIPANLP-ETMTEIRLELNGIKSIPPGAFSPYKLRRLD 340  
 QY 109 QNNKIKEIKENDFKGLTSLYGLIINNKKLTKIHPKAFITTKLRRLYLSHNSLSEI---P 165  
 Db 341 SNNQIAELAPAFQGLRSLNSLVLYGNKIIDTLPRGVGGLYTLQLLLNANKINCIPDA 400  
 QY 166 LNLPKSLAELRIHENVKVKIKQDFTKGMNALHVLMSANP-----LDNNGIE 212  
 Db 401 FQDLQNLNLLSLYDNKIQSLAKGFTSLRAIOTLHLAQNPFICDNLKWLADFLRTNP 460  
 QY 213 -PGA-----FEGVTVEH----- 223  
 Db 461 TTGARCASPRLANRIGQIKSKFRCSAKEQYIPGTEDYHLNSETSDVACPHKCRCE 520  
 QY 224 ---TRIAPAKLTSVPKGLPPTLLEHLHDYNKISTVELED-FKRYKELQRLGLGNKIIDTI 279  
 Db 521 ASVVECSGLKLSKIPERIPQSTTELRLNNNEISILEATGLFKLSHLKLNLSNNKYS 580  
 QY 280 ENGLSIANTPRVREIHLNENKAKIPSGL-PELKYIQIIFLHSIARVGVNDPCPTVPKM 338  
 Db 581 EDGTFEGATSVELHNTANQLESVRSGMFRGLDGLRTMLRNRRISCHNDSETGLRNVR 640  
 QY 339 KKSLY-----SAISIFNPN 352  
 Db 641 LLSLYDNHITTPSGAFDTLQALSTLNLNLP 672

RESULT 19  
 S55275

fibromodulin precursor - human  
 N:Alternate names: 59K collagen-binding matrix protein  
 C:Species: Homo sapiens (man)  
 C:Date: 23-Aug-1995 #sequence\_revision 03-Oct-1995 #text\_change 24-Sep-1999  
 C:Accession: S55275; S35710; S32752; S41925  
 R:Hildebrand, A.; Romaris, M.; Rasmussen, L.M.; Heinegard, D.; Twardzik, D.R.  
 Biochem. J. 302, 527-534, 1994  
 A:Title: Interaction of the small interstitial proteoglycans biglycan, decorin and fi  
 A:Reference number: S55275; MUID:94379985; PMID:8093006  
 A:Accession: S55275  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-376 <HI2>  
 A:Cross-references: EMBL:X75546; NID:g453156; PIDN:CAA53233.1; PID:g453157  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993  
 R:Antonsson, P.; Heinegard, D.; Oldberg, A.  
 Biochim. Biophys. Acta 1174, 204-206, 1993  
 A:Title: Structure and deduced amino acid sequence of the human fibromodulin gene.  
 A:Reference number: S35710; MUID:93363641; PMID:8357838  
 A:Accession: S35710  
 A:Molecule type: DNA  
 A:Residues: 1-3, 'T', 5-86, 'P', 88-209, 'N', 211-225, 'Y', 227-343, 'Q', 345-354, 'M', 356-362, '  
 A:Cross-references: EMBL:X72913; NID:g297090; PIDN:CAA51418.1; PID:g297091  
 C:Comment: Keratan sulfate can be covalently attached to N-acetylglucosamine at the a  
 C:Genetics:  
 A:Gene: GDB:FMOD  
 A:Cross-references: GDB:228979; OMIM:600245  
 A:Map position: 1q32.1-1q32.1  
 A:Introns: 326/2  
 C:Superfamily: fibromodulin; leucine-rich alpha-2-glycoprotein repeat homology  
 C:Keywords: cartilage; chondroitin sulfate proteoglycan; collagen binding; connective  
 F:1-18/Domain: signal sequence #status predicted <SIG>  
 F:19-376/Product: fibromodulin #status predicted <MAT>  
 F:38,39,42,45,47,50,53,55,63,65/Binding site: sulfate (Tyr) (covalent) #status predic  
 F:127,166,201,291/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.08; Score 318; DB 2; Length 376;  
 Best Local Similarity 26.18; Pred. No. 2.2e-14;  
 Matches 86; Conservative 65; Mismatches 131; Indels 48; Gaps 9;

QY 63 SHFFPFDLPF-----CPFGCOC---YSRVVHCSDLG 91  
 Db 37 TYDYPDYPYETYPYCYGVDEGPAYTVGSPDPDPDCECCPPNFLTAMVCDNRN 96  
 QY 92 LTVPTNIPDTRMLDLQNNKIKETKENDFKGLTSLYGLIINNKLTT-KIHPKAFITTK 149  
 Db 97 LKYLPP-VPSRMKYVYFQNNQITSIOGVFDNATGLLWIALHGNQITSDKVGKVFESKLR 155  
 QY 150 KLRRLYLSHNSLSEIPLNLPKSLAELRIHENVKVKIKQDFTKGMNALHVLMSANPLDNN 209  
 Db 156 HLERYLDHNNTLRMPGLPSRLRELHLDHNQISRVNNALLEGLENLTALYLQHDIEI 215  
 QY 210 GTEPGAFEGV-TVFHIRIAEAKLTSVPKGLPPTLLEHLHDYNKISTVELEDFKRYKELQR 268  
 Db 216 G---SSMRGLRSLILLDSYNHLRKPGLPSALEGLYMEHNNVYTPDVSFYGAPKLLY 272  
 QY 269 LGGNKKIIDINGSIA-----NIPRVREIHLNENKAKIPSGLPELKYIQIIFLHSNSTA 324  
 Db 273 VRLSHNSLT---NGLASNTFSNLSLELDLSYNQLOKIP---PVNTLNENLYLOGNRN 326  
 QY 325 RGVGVNDFCPTVPKMKKSLYSALSIFNPNPVK 354  
 Db 327 EFSISFCTVVDVNVFNSKLQVRLDGNKIR 356

RESULT 20  
 B36665

slit protein 2 precursor - fruit fly (Drosophila melanogaster)  
 C:Species: Drosophila melanogaster  
 C:Date: 30-Apr-1991 #sequence\_revision 30-Apr-1991 #text\_change 02-Aug-2002  
 C:Accession: B36665  
 R:Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.  
 Genes Dev. 4, 2169-2187, 1990





QY 207 -----DNNGIEPGA-----PEGVTVFHIRI 226  
 Db 253 PYTCQSPSQLKGVADLHQEFKCSGLTEHAPMECGAENSCHPCRCADGI-----VDC 308  
 QY 227 AEAKLTSPKGLPTLLEHLDYKNTSTVELEDFKRYKELQRLGLGNKTKTDIENGSLAN 286  
 Db 309 REKSLTSVPVTLPTDVTDRLEQNFITELPPKSFSSFRRLRDLNNSNTRIAHDALSG 368  
 QY 287 IPRVREIHLNKKLKKIPSGL-PELKYLIQIIFLHNSIARVGVNDPCPTVPKMKKSLY-- 343  
 Db 369 LKQTLTVLYGNKTKIDPSGVFKGLSLRLLNLANEISCIKRDADF-----RDHLSL 420  
 QY 344 SAISLFPNPKVYWMQPAFTFCVLSRMSVOL 374  
 Db 421 SLLSLYDNNIQ--SIANGTTFAMKSMKTVHL 449

RESULT 22  
 A58532  
 glial cell membrane glycoprotein LIG-1 precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 11-Apr-1997 #sequence\_revision 11-Apr-1997 #text\_change 05-Nov-1999  
 C:Accession: A58532  
 R:Suzuki, Y.; Sato, N.; Tohyama, M.; Wanaka, A.; Takagi, T.  
 J. Biol. Chem. 271, 22522-22527, 1996  
 A:Title: cDNA cloning of a novel membrane glycoprotein that is expressed specifically in  
 A:Reference number: A58532; MUID:96394313; PMID:8798419  
 A:Accession: A58532  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1091 <SUZ>  
 C:Cross-references: GB:D8752; NID:g1545806; PIDN:BAAL1416.1; PID:g1545807  
 C:Superfamily: leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan amino-ter  
 F:36-61/Domain: proteoglycan amino-terminal homology <P>  
 F:71-94/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
 F:95-117/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
 F:118-141/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
 F:142-165/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
 F:166-189/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
 F:191-213/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
 F:214-237/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
 F:238-261/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
 F:262-285/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
 F:286-309/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>  
 F:310-333/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>  
 F:334-357/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>  
 F:358-381/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>  
 F:385-408/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>  
 F:409-432/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>  
 F:440-485/Domain: proteoglycan carboxyl-terminal homology <PCH>

Query Match 14.9%; Score 296; DB 2; Length 1091;  
 Best Local Similarity 30.1%; Pred. No. 2.8e-12;  
 Matches 94; Conservative 64; Mismatches 124; Indels 30; Gaps 12;

QY 74 CPFGCCYRVVHSGDGLGTSVPTNIPFDTMRMLDQNNKTKETKENDFKGLTSLYGLILN 133  
 Db 43 CAAACTCAGNSLDCSGRLATLPDLPSWTRSLNLSYNRLSEIDSAFAEDLTNLQEVYLN 102  
 QY 134 NKLTKTHPKAFLLTKRLRYLSHNLSEI--PMLPKSLAEFLRHENKVKKIQKDF 190  
 Db 103 SNEULTA-PSLGTASIGVWSLFOHNNKLSVDGSQKSYLSVDLSSNNITEIRSSCF 161  
 QY 191 KGMNALHVLMSANPLDNNGT--EPGAFPGV--TVPHIRIABAKLTSVP-KGLP-PTLL 243  
 Db 162 P--NGLRIRELN--LASNRITLESAGFDGLSRSLTLRLSKNRITQLPVKAFKPLRT 216  
 QY 244 ELHLDYKNTSTVELEDFKRYKELQRLGLGNKTKTDIENGSLANIPRVREIHLNKKLKI 303  
 Db 217 QLDLNRNRIRLIEGLTFQGLDSLEVLRLQRNNTSRITDGAFWGLSKMHVHLHLEVNSLIVE 276  
 QY 304 PSG-LPELKYLIQIIFLHNSIARVGVN--DFCPTVPKMKKSLYSALSIFNPNPKVYWMQ 360

Db 277 NSGSLYGLTALHOLHLSNNSISRIQRCWSFC-----QKLHELLISFNNLTRIDEESL 329  
 QY 361 ATRFCVLSRMSV 372  
 Db 330 AE---LSSLSI 337

RESULT 23  
 A53860  
 chondroadherin precursor - bovine  
 N:Alternate names: 38K leucine-rich protein  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 05-Nov-1999  
 C:Accession: A53860  
 R:Neame, P.J.; Sommer, Y.; Boynton, R.E.; Heinegard, D.  
 J. Biol. Chem. 269, 21547-21554, 1994  
 A:Title: The structure of a 38-kDa leucine-rich protein (chondroadherin) isolated fro  
 A:Reference number: A53860; MUID:94342341; PMID:8063792  
 A:Accession: A53860  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-361 <NEA>  
 C:Cross-references: GB:U08018; NID:g470671; PIDN:AAA21330.1; PID:g470672  
 C:Superfamily: leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan carbox  
 C:Keywords: disulfide bond  
 F:300-346/Domain: proteoglycan carboxyl-terminal homology <PCH>

Query Match 14.8%; Score 294; DB 2; Length 361;  
 Best Local Similarity 27.5%; Pred. No. 9.2e-13;  
 Matches 78; Conservative 58; Mismatches 106; Indels 42; Gaps 10;

QY 74 CPFGCCYRVVH--CSDLGLTSTVPTNIPFDTMRMLDQNN----- 111  
 Db 25 CPQNCCHSDLQHVCDKVGLOKIP-KVSEXTKLLNLQRNFPVLATNSFRAMPNLYSLH 83  
 QY 112 ----KIKEIKENDFKGLTSLYGLILNKKLTKIHPKAFLLTKRLRYLSHNLQSEIPLN 167  
 Db 84 LOHCQIREVAGAGFGLKQLIYLYLSHNDIRVLAGAFDDLTLYLYLDHKKVTELPGR 143  
 QY 168 LPKSLAE---LRHKNKVKKIQKDFKGMNALHVLMSANPLDNNIGPEGAFEGV-TVFH 223  
 Db 144 LLSPLNFILOLNNKRIELSGAFQAGKDLRWLYLSENSL--SSLOPGALDDVENLAK 201  
 QY 224 IRIAPAKLTSVPKGLPTLL---ELHLDYKNTSTVELEDFKRYKELQRLGLGNKTKIT 277  
 Db 202 FYLDRNLSSYPSAALSRLRVVEELKLSHNPPLKSPDNAFQSGRY--LETLLDNTNLE 259  
 QY 278 DIENGSLANIPRVREIHLNKKLTKIPSGLPPELKYLIQIIFLHNS 321  
 Db 260 KFDGAFGLVTTLKRVHLENNRLHOLPSNFP-FDSLETTLTLTN 302

RESULT 24  
 T42626  
 secreted leucine-rich repeat-containing protein SLIT2 - mouse (fragment)  
 N:Alternate names: neurogenic extracellular slit protein  
 C:Species: Mus musculus (house mouse)  
 C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 16-Aug-2002  
 C:Accession: T42626  
 R:Holmes, G.P.; Nequs, K.; Burrridge, L.; Raman, S.; Algar, E.; Yamada, T.; Little, M.  
 Mech. Dev. 79, 57-72, 1998  
 A:Title: Distinct but overlapping expression patterns of two vertebrate slit homologs  
 A:Reference number: 222177; MUID:99279238; PMID:10349621  
 A:Accession: T42626  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1025 <HOL>  
 C:Cross-references: EMBL:AF074960; NID:g4151258; PID:g4151259; PIDN:AAD04345.1  
 C:Genetics:  
 A:Gene: Slit2  
 C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein



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A;Reference number: JC6128; MUID:96413591; PMID:8816745

A;Accession: JC6128

A;Molecule type: DNA

A;Residues: 1-603 <BOI>

A;Cross-references: GB:U66900; NID:g1621612; PIDN:AAB17270.1; PID:g1621613

C;Comment: This protein is a serum protein and it is of the ternary complex

C;Genetics:

A;Gene: als

A;Map position: 17

Query Match 13.3%; Score 265; DB 2; Length 603;

Best Local Similarity 27.6%; Pred. No. 1.7e-10;

Matches 88; Conservative 64; Mismatches 103; Indels 64; Gaps 12;

QY 102 DTRMLDLONNKIKKIKENDEKFGTSLTSLVGLLNKNTKTHKRAFLTKKLRRLYLSHNOL 161

DB 219 ELRELDLSRNALSVKRVANVHILPRLOKLYLDRLNLTAVAPRAFLGKMKALRDLDSHNRV 278

QY 162 SEI-----PINL-----PKS-----LAEIRIHENKVKKIKDKTFKGMN 194

DB 279 AGLEEDTFGLLGLHVLRLAHNAITSLRPTPKDLHFLLEQLGHNRIRQLGKTFEGLG 338

QY 195 ALHVLMSANPLDNNGIEPCAFGVTVFHIRIAEK---LTSPV---KGLPPTLLEHL 247

DB 339 QLEVLTLNDNQI--HEYKVGAFG--LFNVAVMNLGNCILRSLPERHVQGL-GRULSHLH 393

QY 248 DYNKISTVELEDEKRYKELQRLGLGNKNTIDENGSLANIPRVRETHLENNKIKKIP--- 304

DB 394 EHSCLGIRLHTTAGLSGLRLERLDRNSISSIEQSLAGLSLELDELDTANQLTHLPQL 453

QY 305 -SGLPEIKYLIQIIFLHNSNIARVGNDFCP-----TVPKMKKSLYSA----- 345

DB 454 FOGLGQLEYL---LLSNQNTMLSEDVLGPLQRAFWLDLSHNRLETPAEGLFSSGLRLRY 510

QY 346 ISLFNNPVKYWEQPATFR 364

DB 511 LNLNRNSLQTFVPQGLER 529

RESULT 28

T13174

gpl50 protein - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 17-Nov-2000

C;Accession: T13174

R;Tian, S.S.; Zinn, K.

J. Biol. Chem. 269, 28478-28486, 1994

A;Title: An adhesion molecule-like protein that interacts with and is a substrate for a

A;Reference number: Z17630; MUID:95050638; PMID:7961789

A;Accession: T13174

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1051 <TIA>

A;Cross-references: EMBL:U15220; NID:g595859; PID:g595860; PIDN:AAA61796.1

A;Experimental source: strain Oregon R

C;Genetics:

A;Cross-references: FlyBase:FBgn0013272

A;Map position: 2

Query Match

Best Local Similarity 13.3%; Score 265; DB 2; Length 1051;

Matches 98; Conservative 51; Mismatches 146; Indels 66; Gaps 12;

QY 35 EDTDDDDDDDDDDDD---DEDSLSLFTPREPRSHFFEDLFPMPFCQCYSR-----VVH 86

DB 203 EGLDDDDDDDDDAADLLTDEQVVFSDVP-----CPFCQCARNVNSYLVA 250

QY 87 CS-----DLGTSVPTNTPF-----DTRMLDLONNKIKKIKEN 119

DB 251 CSRDLMDGIQFGSDITDLVTVNVPKYPILMGNFQNLGKNVASIKTANCTLEYLHAE 310

QY 120 DFKGLTSLYGLIILNNKTKIHKPAFLTTKKLRRLYLSHNQLSEIP-----LNLPRSLAEL 175

DB 311 AFHGLNELYAVNLTDVGLAIINPDFTVGNKKRLMLTISGNDLSVMSSIHLLKSSSIEEL 370

QY 176 RIHENKVKKIOKDTFKGMNALHVLMSANPLDNNGIEPGAFEGVTVF-HIRIAEAKLTSV 234

DB 371 DFSRNNMELNPKAFSHLSNVVYINLSONSLKK--LPEKAFKVTLLLEEDLSVNSLTSL 428

QY 235 PKGL--PPTLELHLDYKNKISTVELEDEKRYKELQRLGLGNKNTIDENGSLANIPRVRE 292

DB 429 PRDIFNGTTLTSLHLKYN--TFNGDLHFGTKDLQQLDLSFNSIVQVHHSFMDRMPGLTN 485

QY 293 IHLNNKLLKKI-PSGLPELKYLIQIIFLHNSNIARVGNDFCPVPMKKKSLYSAISLFINN 351

DB 486 LNLKNGIKKIQDPDSFUTLKLNRHIDUSINDLDQISGMJF-----PKNSELDVIRLNDN 539

QY 352 P 352

DB 540 P 540

RESULT 29

JG0193

G protein-coupled receptor FEX - mouse

C;Species: Mus musculus (house mouse)

C;Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 11-May-2000

C;Accession: JG0193

R;Hermey, G.; Methner, A.; Schaller, H.C.; Hermans-Borgmeyer, I.

Biochem. Biophys. Res. Commun. 254, 273-279, 1999

A;Title: Identification of a novel seven-transmembrane receptor with homology to glyc

A;Reference number: JG0193; MUID:99121227; PMID:9920770

A;Accession: JG0193

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-907 <HER>

Query Match 13.1%; Score 261.5; DB 2; Length 907;

Best Local Similarity 21.8%; Pred. No. 5e-10;

Matches 99; Conservative 68; Mismatches 127; Indels 161; Gaps 14;

QY 69 DLFPN-CPFGQCQY--SRV---VHCSDLGTSVPTNIPFDTRMLD----- 107

DB 28 DAIPRGCFCHCHCELDGRMLLRVDCSDLGSELPSNLSVFTSYLDSMNNISQLPASLH 87

QY 108 -----LONNKIKEIKENDPKGLTSLYGLIINN 134

DB 88 RLCLFLEELRLAGNALTHIPKGAFTGLHSLKVLMLQNNQLRPVPEALQNLRSLSRLIDA 147

QY 135 NKLTIKIHPKAFITTKLRRLYLHSHNQLSEIPLNLPKSLAELR----- 176

DB 148 NHISYVPPSCFSGHSLRHLWLDNALDVPVQAFRSLSALQAMTLALNKTHHIADYAFG 207

QY 177 -----IHENKVKKTQKDTFKGMNALHVLMSANPLD-----NN 209

DB 208 NLSSLVVHLHNNRIHSLGKKCFDGLHSLFTLDLNNYNNLDEFPTAIRTLSNLKELGFHSN 267

QY 210 GT-----EPGAFEGVTVFH----- 223

DB 268 NIRSIPERAFVGNPSLIITHEVDNPIQFVGVSFAFOHLPRLTLTLINGASHITEPPLTGT 327

QY 224 -----IRIAEAKLTSPKGL---PPTLLELHLDYKNKISTVELEDEKRYKELQRLGLGNK 275

DB 328 ATLESLTGTGAKISSLPQAVCDQLPNQVLDLSYNLLE--DLPSLSGCQKLOKIDLRHNE 385

QY 276 ITDIENGSLANIPRVRETHLENNKLLKI-PSGLPELKYLIQIIFLHNS---SIARVGVNDF 331

DB 386 IYEIKGSTFQQLFNLRSLNLANWKIATLHPNAFSTLPSLIKLDLSSNLLSFPVTGLHGL 445

QY 332 CPTVPKMKKSLYSAISLFINN--VKYWEQPATFR 365

DB 446 THLKITGNRALQSLPSANFPKELTIEM-PSAYQC 479

RESULT 30

T19939



## RESULT 33

S72271  
 proteoglycan Lb precursor - mouse  
 N:Alternate names: chondroitin/dermatan sulfate proteoglycan  
 C:Species: Mus musculus (house mouse)  
 C:Date: 14-Apr-1998 #sequence\_revision 24-Apr-1998 #text\_change 20-Jun-2000  
 C:Accession: S72271  
 R:Kurita, K.; Shinomura, T.; Ujita, M.; Zako, M.; Kida, D.; Iwata, H.; Kimata, K.  
 Biochem. J. 318, 909-914, 1996

A:Title: Occurrence of PG-Ib, a leucine-rich small chondroitin/dermatan sulphate proteoglycan in the rat  
 A:Reference number: S72271; MUID:96433109; PMID:8836137

A:Accession: S72271

A:Molecule type: mRNA

A:Residues: 1-322 <KUR>

A:Cross-references: EMBL:D78274; NID:g1620004; PIDN:BAAL1337.1; PID:g1620005

A:Experimental source: strain BALB/c; newborn; epiphyseal cartilage

C:Function:

C:Description: probably participates in ossification process

C:Superfamily: osteoinductive factor precursor; leucine-rich alpha-2-glycoprotein repeat

C:Keywords: glycoprotein

F:1-25/Domain: signal sequence #status predicted <SIG>

F:26-322/Product: proteoglycan Lb #status predicted <WAT>

F:145-167/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>

F:168-191/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>

F:192-211/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>

F:212-237/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>

F:238-258/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>

F:259-282/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>

F:283-302/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.5%; Score 249; DB 2; Length 322;

Best Local Similarity 27.9%; Pred. No. 9.2e-10;

Matches 77; Conservative 47; Mismatches 108; Indels 44; Gaps 9;

Qy 41 DDDDDDDDDNSLFTPTREPRSHFFPDL-----FPMCPGCCQCYSRVHCSDGLT 93

Db 78 DNQEDKDEESTPLRDLGSSQPEEPFGLGPHNTNEFPTCLL-CTCISTVYVCDHED 136

Qy 94 SVPTNIPDTRMLDQNNKKEIKENDFKGLTSLYGLILNANNKLTTHPKAFLTKTLRR 153

Db 137 AIPP-LPKTTFYFSRNRKIKNKNDPASFNLKRLDLSNLSISEDEDAFKLPHLQE 195

Qy 154 LYLHSHNQLSEIPLNPKSLAELRIHENKV--KKIQKDTFGKMAHVLHNSANPLDNGGI 211

Db 196 LVLHONKIKQLP-ELPNTLTFIDISNNRGRGKIGKQAEKDMYDLHLYITDNSLDH-- 251

Qy 212 EPGAEGVTVFHRIAIAEAKLTSVPKGLPPTLLEHLHDYKISIVLEDFPKYKELQRLGL 271

Db 252 -----IPLPLFESRALHQLQNDILEMHEDTFCNVKNLTYV-- 287

Qy 272 GNNKITDIE-NGSLANIPRVREIHLNENKLIKIPSG 306

Db 288 -KALEDIRLDGPNILNLSRTPQAYM---CLPRLPIG 319

RESULT 34

A41915

insulin-like growth factor-binding complex acid-labile chain precursor - human

N:Alternate names: Acid-Labile Subunit (ALS)

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 05-Nov-1999

C:Accession: A41915

R:Leong, S.R.; Baxter, R.C.; Camerato, T.; Dai, J.; Wood, W.I.

Mol. Endocrinol. 6, 870-876, 1992

A:Title: Structure and functional expression of the acid-labile subunit of the insulin-in-

A:Reference number: A41915; MUID:92357025; PMID:1379671

A:Accession: A41915

A:Status: preliminary

A:Molecule type: mRNA;

A:Residues: 1-605 <LEO>

A:Cross-references: GB:M86826; NID:g184807; PIDN:AAA36047.1; PID:g184808

A:Experimental source: liver

C:Note: sequence extracted from NCBI backbone (NCBIP:110171)

C:Superfamily: leucine-rich alpha-2-glycoprotein repeat homology

F:75-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>

F:99-122/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>

F:123-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>

F:147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>

F:171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>

F:195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>

F:219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>

F:243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>

F:267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>

F:291-314/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>

F:315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>

F:339-362/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>

F:363-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>

F:387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>

F:411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>

F:435-458/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>

F:459-482/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR17>

F:483-506/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR18>

F:507-529/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR19>

Query Match 12.3%; Score 246; DB 2; Length 605;

Best Local Similarity 25.3%; Pred. No. 3.4e-09;

Matches 80; Conservative 61; Mismatches 133; Indels 42; Gaps 9;

Qy 72 PMPGFCQCY-----SRVVHCGSDGLTSVPTNIPDTRMLDQNNKIKETKENDFKGIT 125

Db 39 PACPAACVCSYDDADELSVFCSSRNLTPLDGVGGTQALWLDGNNLSVPPAFAQNL 98

Qy 126 SYGLTLNNKNTKTHPKAFLTKKRLRYLHSHNLSIPLNL---PKSLAELRIHENKV 182

Db 99 SLGFLNLQGGQLGLEPQALLGLENLCHLHLERNQLRSALGTFAHTPALASLGSNNRL 158

Qy 183 KTKQDITFGKMAHVLHNSANPLDNGIETP-GAEGVTVFHRIAIAEAKLTSVPKGLPPT 241

Db 159 SLRDLGFLGGLSDMLNIGWNSL---AVLPDAAPRGL-----GS 195

Qy 242 LLEHLHDYKISIVLEDFPKYKELQRLGLGNKNTIDENGLANIPRVREIHLNENKLIK 301

Db 196 LRELVLGNRLAYLPALPFGSLAELRELDLSRNALRAIKANVFVOLPRLOKLYLDRLNIA 255

Qy 302 KI-PSGLPELKYLIQIIFLHNSIARVGVNDPCTVPKMKKSLYSALSIFNPNVKTWQOP 360

Db 256 AVAPCAFLGLKALRWLDLSHNRVAGL-LEDTPFGLGLR-----VLRSLHNAIA--SLRP 307

Qy 361 ATRFCVLSRMSVOLGN 376

Db 308 RTFKDLHFLLEELQLGH 323

RESULT 35

S42799

garp precursor - human

C:Species: Homo sapiens (man)

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jul-2000

C:Accession: S42799; I37407

R:Birnbaum, D.

submitted to the EMBL Data Library, July 1993

A:Reference number: S42799

A:Accession: S42799

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-662 <BIR>

R:Ollendorff, V.; Noguichi, T.; deLapeyriere, O.; Birnbaum, D.

Cell Growth Differ. 5, 213-219, 1994

A:Title: The GARP gene encodes a new member of the family of leucine-rich repeat-cont

A:Reference number: I37407; MUID:94235567; PMID:8180135

A:Accession: I37407

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-662 <RES>

A:Cross-references: translated from GB/EMBL/DBJ



QY 166 LNLPRSLAE-----LRIHENKVKKIQDKDFAGMNAL 190

Db 300 KGLLRLEQLLVLDLSCNQLTSHVDNSTFAGLRLVLNLSNALTRIGSKTFKELYFL 359  
 QY 197 HVLEMSANPLDNNGIEPCAFEGVTVFHIRTAEAKLTSVPKGLPPTLLEHLHDYKNKISTVE 256  
 Db 360 QILDMRNSIGH--IEEGAFPLYNLH-----TLNLAENRLHTLD 397  
 QY 257 LEDEFKRYKELQRLGKNNKTTDIENGSLANIPRVREIHLNENKLLKIPSGLPKELYQII 316  
 Db 398 NRIFNGLYVLTKLTNNLNLVSIIVESAQFRNCSDLKELDLSNQLTEVPEAVQDLSMLKTL 457  
 QY 317 FLHNSIARVGVNDF 331  
 Db 458 DLGENQISEFKNNTF 472

RESULT 41  
 Tl3887  
 tlr protein - fruit fly (Drosophila melanogaster)  
 C:Species: Drosophila melanogaster  
 C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 17-Nov-2000  
 C:Accession: Tl3887  
 R:Chiang, C.; Beachy, P.A.  
 Mech. Dev. 47, 225-239, 1994  
 A:Title: Expression of a novel Toll-like gene spans the parasegment boundary and contrib  
 A:Reference number: Z17805; MUID:95151581; PMID:7848670  
 A:Accession: Tl3887  
 A:Status: preliminary; translated from GB/EMBL/DBDJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1385 <SIE>  
 A:Cross-references: EMBL:S76155; NID:g913247; PID:g913248; PIDN:AAB33383.1  
 C:Genetics:  
 A:Cross-references: FlyBase:Fbgn0004364  
 A:Note: tlr

Query Match 11.2%; Score 223.5; DB 2; Length 1385;  
 Best Local Similarity 25.9%; Pred. No. 3.4e-07;  
 Matches 66; Conservative 42; Mismatches 96; Indels 51; Gaps 3;  
 QY 106 LDLONNKIKETKENDFKGLTSLYGLIINNKKLTIHPKAPLTKKLRRLYLSNQLSEIP 165  
 Db 240 LSLQHNNTIAPNALAGLSRLVNTSYNHLVSLPSEAFAGNKEURELHLOGNDLYELP 299  
 QY 166 LNLPKSLAE-----LRIHENKVKIKQDKFKGMNAL 196  
 Db 300 KGLLRLEQLLVLDLSCNQLTSHVDNSTFAGLRLVLNLSNALTRIGSKTFKELYFL 359  
 QY 197 HVLEMSANPLDNNGIEPCAFEGVTVFHIRTAEAKLTSVPKGLPPTLLEHLHDYKNKISTVE 256  
 Db 360 QILDMRNSIGH--IEEGAFPLYNLH-----TLNLAENRLHTLD 397  
 QY 257 LEDEFKRYKELQRLGKNNKTTDIENGSLANIPRVREIHLNENKLLKIPSGLPKELYQII 316  
 Db 398 NRIFNGLYVLTKLTNNLNLVSIIVESAQFRNCSDLKELDLSNQLTEVPEAAQDLSMLKTL 457  
 QY 317 FLHNSIARVGVNDF 331  
 Db 458 DLGENQISEFKNNTF 472

RESULT 42  
 T42998  
 Ras-binding protein SUR-8 - Caenorhabditis elegans  
 N:Alternate names: leucine-rich repeat protein  
 C:Species: Caenorhabditis elegans  
 C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 21-Jul-2000  
 C:Accession: T42998; T43192  
 R:Selfors, L.M.; Schutzman, J.L.; Borland, C.Z.; Stern, M.J.  
 Proc. Natl. Acad. Sci. U.S.A. 95, 6903-6908, 1998  
 A:Title: Soc-2 encodes a leucine-rich repeat protein implicated in fibroblast growth fac  
 A:Reference number: Z22280; MUID:98284030; PMID:9618511  
 A:Accession: T42998  
 A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA  
 A:Residues: 1-559 <SIE>  
 A:Cross-references: EMBL:AF054827; NID:g3293317; PIDN:AAC25697.1; PID:g3293318  
 R:Sieburth, D.S.; Sun, Q.; Han, M.  
 Cell 94, 119-130, 1998  
 A:Title: SUR-8, a conserved Ras-binding protein with leucine-rich repeats, positively  
 A:Reference number: Z22331; MUID:98337190; PMID:9674433  
 A:Accession: T43192  
 A:Status: preliminary; translated from GB/EMBL/DBDJ  
 A:Molecule type: mRNA  
 A:Residues: 1-559 <SIE>  
 A:Cross-references: EMBL:AF068919; NID:g3252976; PIDN:AAC39129.1; PID:g3252977  
 C:Genetics:  
 A:Gene: soc-2

Query Match 11.2%; Score 223; DB 2; Length 559;  
 Best Local Similarity 24.9%; Pred. No. 1.1e-07;  
 Matches 84; Conservative 67; Mismatches 108; Indels 78; Gaps 14;  
 QY 81 YSRVHVCSO-LGLTSPVPTNIPFTRMLDQNNKIKETKENDFKGLTSLYGLIINNKKLTK 139  
 Db 174 YNRIVAVDEQIGNLS-----KLKMLDVRENKIRELPSAIGK-LTSLVWCLVSYNHLTR 225  
 QY 140 IHPKAPLTKKLRRLYLSNQLSEIPNLNPK--SLAELRIHENKVKIKQD----- 188  
 Db 226 V-PEEIGDCHSLTQLDLQHNLSLPSYSGIKLVNLVRIGIRYNKIRCIPESELESQOOLEE 284  
 QY 189 -----TFKGMNALHVLEMSANPL-----DNNGIEP-- 213  
 Db 285 FIVESNHLQLLPPNLTMLPKIHTVNLRSNELTAFAPGQPOQFVSTVTINMEHNOISKIP 344  
 QY 214 -CAFEGVT-VFHRTAEAKLTSVP--KGLPPTLLEHLHDYKNKISTVEDEFKRYKELQRL 269  
 Db 345 IGIFSKATRLTKLNKRENLVSLPLDMGSWTSITELNSTNOLKVLPE-EDIEKLVNLEIL 403  
 QY 270 GLGNKITDIENGSLANIPRVREIHLNENKLLKIPSGLPKELYQIIIFHNSI----- 323  
 Db 404 VLSNNQKKLPN-QIGLNKRLDELDENELETVPTEIGFLOHLTKLWVQSNKILTPRS 462  
 QY 324 -----ARGVNDPCTVPKMKKSLYSALSLENN 351  
 Db 463 IGNLCSLODLRLGNNL-TAIPETIGHLDSLKSLYN 498

RESULT 43  
 T23841  
 hypothetical protein M88.6b - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T23841  
 R:Sulston, J.  
 submitted to the EMBL Data Library, June 1994  
 A:Reference number: Z19806  
 A:Accession: T23841  
 A:Status: preliminary; translated from GB/EMBL/DBDJ  
 A:Molecule type: DNA  
 A:Residues: 1-594 <WIL>  
 A:Cross-references: EMBL:Z34802; PIDN:CAB54282.1; GSPDB:GN00021; CESP:M88.6b  
 A:Experimental source: clone M88  
 C:Genetics:  
 A:Gene: CESP:M88.6b  
 A:Map position: 3  
 A:Introns: 40/3; 60/2; 101/3; 216/2; 290/1; 361/1; 411/3; 455/1; 544/3

Query Match 11.2%; Score 223; DB 2; Length 594;  
 Best Local Similarity 26.1%; Pred. No. 1.2e-07;  
 Matches 74; Conservative 59; Mismatches 109; Indels 42; Gaps 8;  
 QY 59 REPRSHFFPDLFPMCPFCQCQYRVVHSDLGLTSVPTN----IPFDFRMLDLQNNKTK 114  
 Db 87 RDSVNVLPQDLFE-----NVFAKQVKLERCGLSLTQPNFSQSLGSAELLSRENRIK 140  
 QY 115 EIKENDFKGLTSLYGLIINNKKLTIHPKAPLTKKLRRLYLSHNSLSEIPNL---PKS 171









Db 172 -----VDLSNNSLTQILPGLTINLTNLTNTHLYLHNNKFTFIPEQSF 212  
QY 309 ELKYLIQIFLHNS-----SIARGVNDPCPTVPK 337  
Db 213 QLLQLQETTLNHNWSCDHKONITYLLKWMETKAHVIGIPCSKQVSSLEKESQMYPTPG 272  
QY 338 MKKSIY-----SAISLFNPP-----VKYEMQPATFRCVLSR 369  
Db 273 FTSSLFMTSEMOTVDTINLSMVTQPKVTKPKOYRGKETTFGVTLTK 320

RESULT 49  
Ad1822  
leucine-rich-repeat protein [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp.  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 30-Jun-2002  
C:Accession: Ad1822  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, R.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: Ad1822  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1119 <KUR>  
A:Cross-references: GB:BA000019; PIDN:BA077648.1; PID:g17135102; GSPDB:GN00179  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: alr0124

Query Match 10.9%; Score 216.5; DB 2; Length 1119;  
Best Local Similarity 30.7%; Pred. No. 7.7e-07;  
Matches 77; Conservative 47; Mismatches 94; Indels 33; Gaps 10;

QY 92 LTSVP-----TNIPFTRMLDLQNNKKEIKENDFKGLTSLYGLIINNKKLKIHPKAF 145  
Db 161 ITEPEALAKUTNL-----TQNLNSYNQITEPEALAK-LTNLTQNLNLRGNQRTETI-PEAL 214  
QY 146 LTTKKLRRLYLSHNSLSEIPLNLPK--SLAELRIHENKVKKIQDKTFKGMNALHVLMSA 203  
Db 215 AKLTNLTNLNSYNQRTETIPEALAKLNTQILSDNQIKETIETIAKLTNLTNLI-LSG 273  
QY 204 NPLDN-----NGIEPAGFVTVTHIRIAEAKLSVPGKLPPTLLELHLDYNNKISTV 255  
Db 274 NQIKEIPETIAKLTNLTQILSDNQIKETIPEALAKLTN-----LTQLGLDGNQIKETI 325  
QY 256 ELEDPKRYKELQRLGLGNKKTIDTENGSLANIPRVREIHLNENKLLKIPSCLPKYLQI 315  
Db 326 P-EATKLTNLTNLTSLGNSQIKETIPEALAKLTNLTQILSSNOITEPEVLQTLNLTQ 383  
QY 316 IFLHNSIARV 326  
Db 384 LFLSSNQITQI 394

RESULT 50  
S46224  
peroxidase - fruit fly (Drosophila sp.)  
C:Species: Drosophila sp.  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Oct-2000  
C:Accession: S46224  
R:Nelson, R.E.; Fessler, L.I.; Takagi, Y.; Blumberg, B.; Keene, D.R.; Olson, P.F.; Parkes, E.M.B. J. Biol. Chem. 268, 3438-3447, 1993  
A:Title: Peroxidase: a novel enzyme-matrix protein of Drosophila development.  
A:Reference number: S46224; MUID:94341255; PMID:8062820  
A:Accession: S46224  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1535 <NEL>  
A:Cross-references: GB:U11052; NID:g531384; PIDN:AAA61568.1; PID:g531385  
C:Supfamily: peroxidase; myeloperoxidase homology; proteoglycan amino-terminal homolo

F:19-44/Domain: proteoglycan amino-terminal homology <PAH4>  
F:661-1350/Domain: myeloperoxidase homology <MPX>

Query Match 10.8%; Score 215.5; DB 2; Length 1535;  
Best Local Similarity 32.5%; Pred. No. 1.4e-06;  
Matches 55; Conservative 25; Mismatches 56; Indels 33; Gaps 4;

QY 74 CPFGCQCYSRVVHCSDGLTSVPTNIPEDTRMLDLQNNKKEIKENDFKGLTSLYGLIIN 133  
Db 26 CPAGCTCLERTVRCIRAKLSAVP-KLPQDTQTDLRFNHIEELPANAFSGLAQLTTLFLN 84  
QY 134 NNKLTIKIHPKAFITTKLRRLYLSHNSLSEIPL----- 166  
Db 85 DNELAYLDQALNGLTALRFVYLLNNNRLSRLPATITFORMPRLEGITFLENNDIWQLPAGLF 144  
QY 167 -NLPKSLAELRIHENKVKKIQDKTFKGMNALHVLMSANPLD---NNGI 211  
Db 145 DNLPR-LNRLIMYNNKLTQLPVDGFRNLNKLRLDGNNAIDIDCNCGV 192

Search completed: January 24, 2003, 12:27:32  
Job time : 29 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 24, 2003, 12:21:30 ; Search time 14 Seconds  
(without alignments)  
1122.823 Million cell updates/sec

Title: US-09-944-457-2

Perfect score: 1992

Sequence: 1 MKEYVLLFLALCSAKPFPS.....PATFRCLVSRMSVQLGNFGM 379

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	1992	100.0	379	1	ASPN_HUMAN		Q9bxx1 homo sapien
2	1799	90.3	373	1	ASPN_MOUSE		Q99mq4 mus musculus
3	1044	52.4	368	1	PGS1_XENLA		Q9ib75 xenopus lae
4	1040.5	52.2	369	1	PGS1_RAT		Q47853 rattus norv
5	1037.5	52.1	369	1	PGS1_MOUSE		Q28553 mus musculus
6	1034	51.9	368	1	PGS1_HUMAN		Q21810 homo sapien
7	1028.5	51.6	372	1	PGS1_HORSE		Q46403 equus cabal
8	1027.5	51.6	369	1	PGS1_SHEEP		Q46390 ovis aries
9	1021.5	51.3	369	1	PGS1_CANFA		Q02678 canis famil
10	1019.5	51.2	369	1	PGS1_BOVIN		Q21809 bos taurus
11	974	48.9	356	1	PGS2_COTJA		Q9de68 coturnix co
12	969	48.6	357	1	PGS2_CHICK		Q28675 gallus gall
13	967	48.5	360	1	PGS2_PIG		Q9xsd9 sus scrofa
14	963.5	48.4	359	1	PGS2_HUMAN		Q07585 homo sapien
15	947	47.5	360	1	PGS2_SHEEP		Q9tte2 ovis aries
16	943	47.3	360	1	PGS2_BOVIN		Q21793 bos taurus
17	941	47.2	360	1	PGS2_RABIT		Q28888 oryctolagus
18	939	47.1	360	1	PGS2_HORSE		Q46542 equus cabal
19	934	46.9	360	1	PGS2_CANFA		Q29393 canis famil
20	907.5	45.6	354	1	PGS2_MOUSE		Q28654 mus musculus
21	899	45.1	354	1	PGS2_RAT		Q01129 rattus norv
22	641	32.2	272	1	PGS1_PIG		Q9gkq6 sus scrofa
23	442	22.2	135	1	PGS1_RABIT		Q46377 oryctolagus
24	399.5	20.1	343	1	LUM_CHICK		P51890 gallus gall
25	398.5	20.0	343	1	LUM_COTJA		Q9de67 coturnix co
26	390	19.6	338	1	LUM_HUMAN		Q9de64 homo sapien
27	384	19.3	342	1	LUM_BOVIN		Q05443 bos taurus
28	383	19.2	338	1	LUM_MOUSE		P51885 mus musculus
29	378	19.0	338	1	LUM_RAT		P51886 rattus norv
30	366	18.4	421	1	OMD_HUMAN		Q99983 homo sapien
31	363.5	18.2	646	1	FRL1_HUMAN		Q9nzul homo sapien
32	361.5	18.1	381	1	FRL1_BOVIN		Q9gkn8 bos taurus
33	358.5	18.0	382	1	PRLP_HUMAN		P51888 homo sapien

## ALIGNMENTS

### RESULT 1

ID	ASPN_HUMAN	STANDARD:	PRT;	379 AA.
AC	Q9BXN1; Q96LD0; Q96K79;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Asporin precursor (Periodontal ligament associated protein-1) (PLAP-1).			
DE	1).			
GN	ASPN OR PLAPI.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. PARTIAL SEQUENCE, CARBOHYDRATE-LINKAGE SITE			
RP	ASN-281, MASS SPECTROMETRY, AND POLYMORPHISM OF POLY-ASP REGION.			
RC	TISSUE=Cartilage;			
RX	MEDLINE=21192276; PubMed=11152692;			
RA	Lorenzo P., Asperberg A., Oennerfjord P., Bayliss M.T., Neame P.J.,			
RA	Heinegaard D.;			
RT	"Identification and characterization of asporin. A novel member of the			
RT	leucine-rich repeat protein family closely related to decorin and			
RT	biglycan.";			
RL	J. Biol. Chem. 276:12201-12211(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=21472263; PubMed=11587855;			
RA	Yamada S., Murakami S., Matoba R., Ozawa Y., Yokokoji T., Nakahira Y.,			
RA	Ikezawa K., Takayama S.-I., Matsubara K., Okada H.;			
RT	"Expression profile of active genes in human periodontal ligament and			
RT	isolation of PLAP-1, a novel SLRP family gene.";			
RL	Gene 275:279-286(2001).			
RN	[3]			
RP	SEQUENCE OF 1-242 FROM N.A.			
RC	TISSUE=Embryo;			
RC	Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,			
RA	Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,			
RA	Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,			
RA	Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,			
RA	Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,			
RA	Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y.,			
RA	Ninomiya K., Iwayanagi T.;			
RT	"NEDO human cDNA sequencing project.";			
RL	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	PARTIAL SEQUENCE FROM N.A.			
RP	PubMed=11152695;			
RA	Henry S.P., Takanosu M., Boyd T.C., Mayne P.M., Eberspaecher H.,			
RA	Zhou W., de Crombrughe B., Hoeck M., Mayne R.;			
RT	"Expression pattern and gene characterization of asporin. A newly			

34	356.5	17.9	377	1	PRLP_RAT	Q9eqp5 rattus norv
35	345	17.3	351	1	KERA_MOUSE	Q35367 mus musculus
36	342.5	17.2	375	1	FMOD_BOVIN	F13605 bos taurus
37	342.5	17.2	378	1	PRLP_MOUSE	Q9jk53 mus musculus
38	340.5	17.1	352	1	KERA_BOVIN	O62702 bos taurus
39	340.5	17.1	352	1	KERA_HUMAN	O60938 homo sapien
40	338	17.0	376	1	FMOD_RAT	P50609 rattus norv
41	338	17.0	422	1	OMD_BOVIN	O77742 bos taurus
42	333.5	16.7	380	1	FMOD_CHICK	P51887 gallus gall
43	331.5	16.6	649	1	FLR3_HUMAN	P09nzu0 homo sapien
44	331	16.6	376	1	FMOD_MOUSE	P50608 mus musculus
45	325	16.3	353	1	KERA_CHICK	O42235 gallus gall
46	325	16.3	353	1	KERA_COTJA	O9de66 coturnix co
47	325	16.3	376	1	FMOD_HUMAN	O06828 homo sapien
48	316	15.9	1480	1	SLIT_DROME	P24014 drosophila
49	313.5	15.7	660	1	FLR2_HUMAN	O43155 homo sapien
50	306.5	15.4	423	1	OMD_MOUSE	O35103 mus musculus

Db	61	PRSHFFPFDLPMCPGPCQCVSWVHCSDGLGTSVPTNIPFTRMDLQNNKIKEND	120
QY	121	FKGLTSYGLILNNKLTIKHPKAFUETTKKLRLYLHSHQLSEIPLNLPKSLAEURIHEN	180
Db	121	FKGLTSYGLILNNKLTIKHPKAFUETTKKLRLYLHSHQLSEIPLNLPKSLAEURIHEN	180
QY	181	KVKIKQDFTFGMNAJLVLEMSANPLDNNNGIEBPGAEGVTVFHIRIAEAKLTSVPKGLPP	240
Db	181	KVKIKQDFTFGMNAJLVLEMSANPLDNNNGIEBPGAEGVTVFHIRIAEAKLTSVPKGLPP	240
QY	241	TLLELHLDYNNKISTVELEDFKRYKELORLGLGNKKTTDIEGSLANIPKRVREIHLENNKL	300
Db	241	TLLELHLDYNNKISTVELEDFKRYKELORLGLGNKKTTDIEGSLANIPKRVREIHLENNKL	300
QY	301	KKIPSGLPKLYQLIIFLHNSIARVGVNDFCTVPKMKKSILYSALSLENNPVKYWEMOP	360
Db	301	KKIPSGLPKLYQLIIFLHNSIARVGVNDFCTVPKMKKSILYSALSLENNPVKYWEMOP	360
QY	361	ATFCVLSRMSVOLGNFGM 379	
Db	361	ATFCVLSRMSVOLGNFGM 379	
RESULT 2			
ASPN_MOUSE			
ID	ASPN_MOUSE	STANDARD;	PRT; 373 AA.
AC	Q99MO4; Q9D6A2;		
DC	15-JUN-2002 (Rel. 41, Created)		
DT	15-JUN-2002 (Rel. 41, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Asporin precursor.		
GN	ASPN.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
ON	NCBI_TaxID=10090;		
OX	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6 X 129/SVJ; TISSUE=Aorta;		
RX	MEDLINE=21192276; PubMed=11152892;		
RA	Lorenzo P., Asberg A., Oennerfjord P., Bayliss M.T., Neame P.J.,		
RA	Heinegaard D.;		
RT	"Identification and Characterization of Asporin. A novel member of the		
RT	leucine-rich repeat protein family closely related to decorin and		
RT	biglycan.";		
RT	J. Biol. Chem. 276:12201-12211(2001).		
RN	[2]		
RP	SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGE.		
RX	PubMed=11152695;		
RA	Henry S.P., Takanosu M., Boyd T.C., Wayne P.M., Eberspaecher H.,		
RA	Zhou W., de Crombrughe B., Hoeoek M., Wayne R.;		
RT	"Expression pattern and gene characterization of asporin. A newly		
RT	discovered member of the leucine-rich repeat protein family.";		
RT	J. Biol. Chem. 276:12212-12221(2001).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Skin;		
RX	MEDLINE=21085660; PubMed=11217851;		
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,		
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,		
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,		
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,		
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		
RA	Fleischmann W., Gaasterland T., Glassi C., King B., Kochiwa H.,		
RA	Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,		
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,		
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,		
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,		
RA	Gustincich S., Hill D., Hotman M., Hume D.A., Kamiya M., Lee N.H.,		
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,		
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		

RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Hayashaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohitsuki S.,  
 RA Hayashizaki Y.,  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).  
 CC -!- TISSUE SPECIFICITY: Higher expression in heart, also detected in  
 CC kidney, stomach, testes, and skin but only weakly in lung,  
 CC skeletal muscle, small intestine, and thymus.  
 CC -!- DEVELOPMENTAL STAGE: At 12.5 dpc, it is present in the mandibular  
 CC as well as maxillary components of the first branchial arch. Also  
 CC detected in the thoracic body wall adjacent to the heart. At 13.5  
 CC dpc, it is detected in the mesenchyme lateral to Meckel's  
 CC cartilage. Pronounced expression is observed in the perichondrium  
 CC of the humerus, ribs, and scapula. At 14.5 dpc, it is detected in  
 CC the mesenchymal condensations lateral to Meckel's cartilage, in  
 CC the perichondrium surrounding the central cartilaginous elements  
 CC of the vertebra and also in the dermal mesenchyme. At 15.5 dpc, it  
 CC is expressed in the perichondrium/perioosteum of the long bones  
 CC (i.e. femur, tibia, and fibula), some of the flat bones at the base  
 CC of the skull (i.e. sphenoid bone), ribs, clavicle, and vertebrae.  
 CC Also detected in the intramembranous bones of the maxilla and  
 CC mandible (alveolar bone) and a strong expression is observed in  
 CC sagittal sections of the subcutaneous muscles or panniculus  
 CC carnosus of the thorax, trunk, and head/neck (platysma muscle)  
 CC region. Very little expression is detected in the major  
 CC parenchymal organs (with the exception of the large bronchi of the  
 CC lung). Its expression is prominent in the developing mouse  
 CC skeleton, particularly in the perichondrium/perioosteum of  
 CC cartilage/bone, and is also found in other specialized connective  
 CC tissues such as tendon, sclera, the connective tissue sheath  
 CC surrounding muscle and dermis. In the sclera of the eye it is  
 CC first detected at 15.5 dpc and stronger expression was detected at  
 CC 17.5 dpc.  
 CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS  
 CC (SLRPS) FAMILY. CLASS 1 SUBFAMILY.  
 CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).  
 CC -!- CAUTION: Ref.3 sequence differs from that shown due to a stop  
 CC codon in position 238.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----

DR EMBL; AF316825; AAK35162.1; -  
 DR EMBL; AK014504; BAB29402.1; ALT\_TERM.  
 DR MGD; MGI:1913945; Aspn.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR000372; LRR\_Nterm.  
 DR InterPro; IPR003592; LRR\_out.  
 DR InterPro; IPR003591; LRR\_typ.  
 DR Pfam; PF00560; LRR; 8.  
 DR Pfam; PF01462; LRRNT; 1.  
 DR SMART; SM00370; LRR; 3.  
 DR SMART; SM00013; LRRNT; 1.  
 DR SMART; SM00369; LRR\_TYP; 7.  
 KW Glycoprotein; Extracellular matrix; Signal; Repeat;  
 FT SIGNAL 1 15 POTENTIAL.  
 FT PROPEP 16 32 POTENTIAL.  
 FT CHAIN 33 373 ASPORIN.  
 FT DOMAIN 76 89  
 FT REPEAT 89 109 CYS-RICH.  
 FT REPEAT 110 133 LRR-S 1.  
 FT REPEAT 134 157 LRR-T 1.  
 FT REPEAT 158 178 LRR-T 2.  
 FT REPEAT 179 202 LRR-S 2.  
 FT REPEAT 203 227 LRR-T 3.  
 FT REPEAT 203 227 LRR-T 4.

FT REPEAT 228 248 LRR-S 3.  
 FT REPEAT 249 272 LRR-T 5.  
 FT REPEAT 273 296 LRR-T 6.  
 FT REPEAT 297 319 LRR-S 4.  
 FT REPEAT 320 349 LRR-T 7.  
 FT REPEAT 350 373 LRR-T 8.  
 FT DOMAIN 36 45 POLY-ASP.  
 FT DISULFID 326 359 BY SIMILARITY.  
 FT CARBOHYD 48 48 O-LINKED (BY SIMILARITY).  
 FT CARBOHYD 275 275 N-LINKED (GLNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 373 AA; 42572 MW; A50G4C82AABCF35 CRC64;  
 Query Match 90.3%; Score 1799; DB 1; Length 373;  
 Best Local Similarity 90.2%; Pred. No. 2.5e-117;  
 Matches 341; Conservative 17; Mismatches 14; Indels 6; Gaps 1;  
 QY 1 MKEYVLLFLALCSAKFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDDDDSLFPTR 60  
 DB 1 MKEYVMLLLAVCSAKFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDDDDSLFPTR 54  
 QY 61 PRSHFFFDLPPMCPFCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEND 120  
 DB 55 PVNFFFDLPPMCPFCQCYSRVVHCSDLGLTSVPTNIPFDTRMVDLQNNKIKEIKEND 114  
 QY 121 FKGLTSLYGLTLNNKLTIKHPKAFITTKLRLRLYLSHNSLSEIPLNPKSLAELRTHEN 180  
 DB 115 FKGLTSLYALLNNKLTIKHPKFTLTKLRLRLYLSHNSLSEIPLNPKSLAELRIHDN 174  
 QY 181 KVKKIQTDFKGMNALHVEMSANPLDNGIEPGEFVTFVHRTIAEAKLTSPVKGGLPP 240  
 DB 175 KVKKIQTDFKGMNALHVEMSANPLDNGIEPGEFVTFVHRTIAEAKLTSPVKGGLPP 234  
 QY 241 TLELHLHDYKISTVELEDEKRYKELORLGLGNKKTIDDIENGSLANIPRVRETHLENNKL 300  
 DB 235 TLELHLHDYKISTVELEDEKRYKELORLGLGNKKTIDDIENGSLANIPRVRETHLENNKL 294  
 QY 301 KKIPSGPELKYLIQIFLHNSNARVGVNDFCTVPKMKKSLYSALSFNNPKYVWDMQP 360  
 DB 295 KKIPSGQLKYLQIIFLHNSNARVGVNDFCTVPKMKKSLYSALSFNNPKYVWDMQP 354  
 QY 361 ATFRCVLSRMSVQLGNFG 378  
 DB 355 ATFRCVLSRMSVQLGNVG 372  
 RESULT 3  
 PGSL\_XENLA  
 ID PGSL\_XENLA STANDARD; PRT; 368 AA.  
 AC Q9IB75;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Bglican precursor.  
 GN BGN.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodidae; Xenopus.  
 OC NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Goto T., Kubota H.Y.;  
 RT "cDNA of biglycan of Xenopus laevis.";  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: May be involved in collagen fiber assembly (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).  
 CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS  
 CC (SLRPS) FAMILY. CLASS 1 SUBFAMILY.  
 CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).  
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QY	240	PTLELHLDYKNKISTVELEDFKRYKELORLGLGNKKITDIENGLANIIPRVREIHLNNK	299
Db	230	ETNELHLDHNKQTAELEDDLRYSKDYRUGLGHQNRIMIEGSLFPTLRELHLDNNK	289
QY	300	LKKIPSGELPKYLIQIIFLHNSNIARVGVNDFCTPVPKMKLSYSAISLFNNPVKYWMQ	359
Db	290	LSRYPGLDLKLQVYVYLHNSNITKVGINDCFPMGFGVKRAYNGISLFNPNVPVWEVQ	349
QY	360	PATRCVLSRMSVOLGNF	377
Db	350	PATRCVTDRLAIQFGNY	367

DR	EMBL; X53928; CAA37875.1; -.
DR	EMBL; L20276; AAA64360.1; -.
DR	EMBL; BC005452; AAH05452.1; -.
DR	EMBL; BC019502; AAH19502.1; -.
DR	EMBL; Y11758; CAA72422.1; -.
DR	PIR; S20811; S20811.
DR	MGD; MGI:88158; Bgn.
DR	InterPro; IPR001611; LRR.
DR	InterPro; IPR000372; LRR_Nterm.
DR	InterPro; IPR003592; LRR_Out.
DR	InterPro; IPR003591; LRR_Typ.
DR	Bfam; BF00550; LRR_0

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QY 60 EPRSHPEPDLFPMCPGOCYGRVYHCSDLGLTSVPTNIPFTRMLDQNNKIKKEIKEN 119
Db 60 -----FSAMCPGCHLRVQCSDGLGKTVKPEISPTTLLDQNNDISLRKD 109
QY 120 DFGLTSLYGLIILNNKTKIKHPKAFATTKKRLRLYLSHNQSEIPLNLPKSLAEIUIHE 179
Db 110 DFKGLQHLVALVNNKISKIHEKAFSPRLKQKLYSKNHLVEIPNLPSSILVELRIHD 169
QY 180 NKVKIKQDTEFKGNALHVLSEANPLDNGNIEPGAEGVTVPHIRIAEAKLTSVPKGLP 239
Db 170 NRIRKVPKGVSLRNNNCIEEMGNPLENSGFEPGAFDGLKLNLYLRISAKUTGIPKDL 229
QY 240 PTLLEHLNDYKISTVELEDFKRYKELQRLGLGNKTKITDIENGSLANIPRVRIHLNENK 299
Db 230 ETNELHLDHKNKIOAIELEDLRLRYSKLYRLGLGHQIRMTENGSLFPLTLRELHLDNKK 289
QY 300 LKTPSGLPKELYLIIFLHNSNISTARVGVNDFCTVPKMKKSLYSALSIFNNPVKWEQ 359
Db 290 LSRVPAGLPDLKLVVYLLHSNITKVGINDFCPMGFGVKRAYINGISLFNNPVPYWEQ 349
QY 360 PATERCVLSRMSVOLGNF 377
Db 350 PATERCVTDRLAIOFGNY 367

RESULT 6
PGS1_HUMAN
ID PGS1_HUMAN STANDARD; PRT; 368 AA.
AC P21810; P13247;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Biglycan precursor (Bone/cartilage proteoglycan I) (PG-S1).
GN BGN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN R01171;
RS SEQUENCE FROM N.A.
RC TISSUE=Bone;
EX MEDLINE=89174714; PubMed=2647739;
RA Fisher L.W., Termine J.D., Young M.F.;
RT "Deduced protein sequence of bone small proteoglycan I (biglycan)
RT shows homology with proteoglycan II (decorin) and several
RT nonconnective tissue proteins in a variety of species.";
RL J. Biol. Chem. 264:4571-4576(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91317791; PubMed=1860845;
RA Fisher L.W., Heegaard A.M., Vetter U., Vogel W., Just W.,
RA Termine J.D., Young M.F.;
RT "Human biglycan gene. Putative promoter, intron-exon junctions, and
RT chromosomal localization.";
RL J. Biol. Chem. 266:14371-14377(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20314869; PubMed=10854409;
RA Mallon A.M., Platzer M., Bates R., Gloeckner G., Botcherby M.,
RA Nordsiek G., Strivens M.A., Kioschis P., Dangel A., Cunningham D.,
RA Straw R., Weston P., Hunter C., Gilbert M., Fernando S., Goodall K.,
RA Kerry G., Greystrom J.S., Clark D., Goerdes M., Blechschmidt K.,
RA Kump A., Hinzmann B., Mundy C.R., Miller W., Poustka A., Herman G.E.,
RA Rhodes M., Denny P., Rosenthal A., Brown S.D.M.;
RT "Comparative genome sequence analysis of the Bpa/Str region in mouse
RT and man.";
RL Genome Res. 10:758-775(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [5]

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RP SEQUENCE OF 38-57.
RX MEDLINE=90073579; PubMed=2590169;
RA Roughley P.J., White R.J.;
RT "Dermatan sulphate proteoglycans of human articular cartilage. The
RT properties of dermatan sulphate proteoglycans I and II.";
RL Biochem. J. 262:823-827(1989).
RN [6]
RP SEQUENCE OF 38-66.
RX MEDLINE=87250639; PubMed=3597437;
RA Fisher L.W., Hawkins G.R., Termine J.D.;
RT "Purification and partial characterization of small proteoglycans I
RT and II, bone sialoproteins I and II, and osteonectin from the mineral
RT compartment of developing human bone.";
RL J. Biol. Chem. 262:9702-9708(1987).
RN [7]
RP SEQUENCE OF 361-368 FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=95187185; PubMed=7881444;
RA Just W., Rau W., Muller R., Geerkens C., Vogel W.;
RT "Dinucleotide repeat polymorphism at the human biglycan (BGN)
RT locus.";
RL Hum. Mol. Genet. 3:2268-2268(1994).
CC -!- FUNCTION: May be involved in collagen fiber assembly (By
CC similarity).
CC -!- SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
CC -!- TISSUE SPECIFICITY: Found in several connective tissues, specially
CC in articular cartilages.
CC -!- PTM: The two attached glycosaminoglycan chains can be either
CC chondroitin sulfate or dermatan sulfate (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
CC (SLRPS) FAMILY. CLASS I SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J04599; AAA36009.1; -.
CC EMBL; M65153; AAA52287.1; ALT_SEQ.
CC EMBL; M65152; AAA52287.1; JOINED.
CC EMBL; U82695; AAF33530.1; -.
CC EMBL; BC002416; AAH02416.1; -.
CC EMBL; BC004244; AAH04244.1; -.
CC EMBL; U11686; AAC50117.1; -.
CC PIR; A28457; A28457.
CC PIR; A32458; A32458.
CC PIR; A40757; A40757.
CC PIR; S05639; S05639.
CC Genew; HGNC:1044; BGN.
CC MIM; 301870; -.
CC InterPro; IPR001611; LRR.
CC InterPro; IPR000372; LRR_Nterm.
CC InterPro; IPR003592; LRR_out.
CC InterPro; IPR003591; LRR_typ.
CC Pfam; PF00560; LRR; 8.
CC Pfam; PF01462; LRRNT; 1.
CC SMART; SM00370; LRR; 3.
CC SMART; SM00013; LRRNT; 1.
CC SMART; SM00369; LRR_TYP; 1.
CC Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 37
FT CHAIN 38 368 BIGLYCAN.
FT DOMAIN 63 76 CYS-RICH.
FT REPEAT 82 102 LRR-S 1.
FT REPEAT 103 126 LRR-T 1.

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FT REPEAT 127 150 LRR-T 2.  
 FT REPEAT 151 171 LRR-S 2.  
 FT REPEAT 172 195 LRR-T 3.  
 FT REPEAT 196 220 LRR-T 4.  
 FT REPEAT 221 241 LRR-S 3.  
 FT REPEAT 242 265 LRR-T 5.  
 FT REPEAT 266 289 LRR-T 6.  
 FT REPEAT 290 312 LRR-S 4.  
 FT REPEAT 313 342 LRR-T 7.  
 FT REPEAT 343 368 LRR-T 8.  
 FT CARBOHYD 42 42 O-LINKED (GLYCOSAMINOGLYCAN).  
 FT CARBOHYD 47 47 O-LINKED (GLYCOSAMINOGLYCAN).  
 FT CARBOHYD 270 270 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 311 311 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT DISULFID 63 76 BY SIMILARITY.  
 FT DISULFID 321 354 BY SIMILARITY.  
 FT CONFLICT 139 140 KL -> NV (IN REF. 1).  
 FT CONFLICT 163 164 EL -> DV (IN REF. 1).  
 SQ SEQUENCE 368 AA; 41654 MW; BF16F304C5CD3B3E CRC64;

Query Match 51.9%; Score 1034; DB 1; Length 368;  
 Best Local Similarity 53.2%; Pred. No. 1.6e-64;  
 Matches 200; Conservative 63; Mismatches 93; Indels 20; Gaps 3;

QY 6 ILLFLALCSAKPF-----FSPSHIALKNMMLKDMEDTDDDDDDDDDDDDSDNSLFPPTREP 61  
 Db 7 LVSLALLSQALPFQEGFMDFTLDDGGPPMNDDEASGADTSGVLDPD-----SVTPYIS- 60

QY 62 RSHFFPDLFPMCPFGCOCYSRVVHCSDGLTSTVPTNIPFDTRMLDLQNNKIRKENDF 121  
 Db 61 -----AMCPFGCHLRVQCSDGLKSPKESPDPTLLDLQNNDISLRKDDF 110

QY 122 KGLTSLYGLIINNKKLTHPKAFLLTKKRLRLYLSHNSLSEIPLNPKSLAEIRIHENK 181  
 Db 111 KGLHLYALVLYNNKISKIHEKASPLRKQKLYISKNHVEIPNPLSSLVEIRIHDRN 170

QY 182 VKTKQDFTKGMNALHVLMSANPLDNGIEPGAFEGVTHIRIARAKLTSPKGLPPT 241  
 Db 171 IRKVPKGVGLRNMNCTEMGPNLENSGPEGAFDGLKLYLRISAKLTGPKDLPET 230

QY 242 LLEHLNDYNTSTVEDEFKYKELQRLGLGNKKTIDENGLSANIPRVREIHLNKKL 301  
 Db 231 LNEHLNDHNTQALELDDLRYSLYRLGLGHQIRMIENGLSFLFTLRELHLDNNKLA 290

QY 302 KIPSLPELKYLIQIFLHNSIARVNDPCPTVPKMKKSLYSALSIFNPNVYWEQPA 361  
 Db 291 RVPSSLPDLKLLQVYLLHNSNITKGVNDPCPMGFGVKRAYNGISLFPNPNVYWEQPA 350

QY 362 TFRCLVSRMSVOLGNF 377  
 Db 351 TFRCLVSRMSVOLGNF 366

RESULT 7  
 PGSI\_HORSE STANDARD; PRT; 372 AA.  
 AC 046403; Q9NIU5;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Biglycan precursor (Bone/cartilage proteoglycan I) (PG-S1).  
 GN BGN.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Richardson D.W., Dodge G.R.;  
 RT "Dose dependent effects of corticosteroids on the expression of matrix  
 related genes in equine articular chondrocytes";  
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]

RP SEQUENCE OF 150-192 FROM N.A.  
 RX MEDLINE=20082971; PubMed=10613847;  
 RA Caetano A.R., Shiue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,  
 RA Bowling A.T., Murray J.D.;  
 RT "A comparative gene map of the horse (Equus caballus).";  
 RL Genome Res. 9:1239-1249(1999).  
 CC -!- FUNCTION: May be involved in collagen fiber assembly (By  
 CC similarity).  
 CC -!- SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).  
 CC -!- PTM: The two attached glycosaminoglycan chains can be either  
 CC chondroitin sulfate or dermatan sulfate (By similarity).  
 CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN  
 CC (SLRPS) FAMILY. CLASS I SUBFAMILY.  
 CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).  
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 CC -----  
 DR EMBL; AF035934; AAB89305.1; -;  
 DR EMBL; AF135020; AAF64248.1; -;  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR000372; LRR\_Nterm.  
 DR InterPro: IPR003592; LRR\_out.  
 DR InterPro: IPR003591; LRR\_typ.  
 DR Pfam: PF00560; LRR; 7.  
 DR Pfam: PF01462; LRRNT; 1.  
 DR SMART; SM00370; LRR; 3.  
 DR SMART; SM00013; LRRNT; 1.  
 DR SMART; SM00369; LRR\_TYP; 1.  
 DR KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;  
 KW Leucine-rich repeat; Signal.  
 FT SIGNAL 1 22 POTENTIAL.  
 FT PROPEP 23 40 BY SIMILARITY.  
 FT CHAIN 41 372 BIGLYCAN.  
 FT DOMAIN 67 80 CYS-RICH.  
 FT REPEAT 86 106 LRR-S 1.  
 FT REPEAT 107 130 LRR-T 1.  
 FT REPEAT 131 154 LRR-T 2.  
 FT REPEAT 155 175 LRR-S 2.  
 FT REPEAT 176 199 LRR-T 3.  
 FT REPEAT 200 224 LRR-T 4.  
 FT REPEAT 225 245 LRR-S 3.  
 FT REPEAT 246 269 LRR-T 5.  
 FT REPEAT 270 293 LRR-T 6.  
 FT REPEAT 294 316 LRR-S 4.  
 FT REPEAT 317 346 LRR-T 7.  
 FT REPEAT 347 372 LRR-T 8.  
 FT CARBOHYD 45 45 O-LINKED (GLYCOSAMINOGLYCAN) (BY  
 FT SIMILARITY).  
 FT CARBOHYD 51 51 O-LINKED (GLYCOSAMINOGLYCAN) (BY  
 FT SIMILARITY).  
 FT CARBOHYD 274 274 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 315 315 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT DISULFID 67 80 BY SIMILARITY.  
 FT DISULFID 325 358 BY SIMILARITY.  
 SQ SEQUENCE 372 AA; 41924 MW; D0BBF8576C5F082E CRC64;

Query Match 51.6%; Score 1028.5; DB 1; Length 372;  
 Best Local Similarity 52.4%; Pred. No. 3.9e-64;  
 Matches 198; Conservative 67; Mismatches 94; Indels 19; Gaps 3;

QY 4 YVLLFLALCSAKPF-----FSPSHIALKNMMLKDMEDTDDDDDDDDDDSDNSLFPPT 59  
 Db 8 WLIALSLLSQALPFQEGFMDFTLDDGGPPMNDDEASGADTSGIPDJD-----SLTPT- 62

QY 60 EPRSHFFPDLFPMCPFGCOCYSRVVHCSDGLTSTVPTNIPFDTRMLDLQNNKIRKEND 119

Db 63 -----FSAMCPGCHLRVVCQSDGLGKAVPKEISPDPTTLLDQNNSEISLRKD 112  
 QY 120 DFKGLTSLYGLIINNNKLTTHKPAFLTTKRLRLYLSHNOLSEIPLNLPKSLAEIRIHE 179  
 Db 113 DFKGLQHLVLYLVNNKISIKHEKAFSPLRKRLQKLYISKNLHVEIPNLPSSVLRLIHD 172  
 QY 180 NKVKIKQKDTFKGMALHVLSEMSANPLDNNNGIEPFAFEGVTVPFHRIAEAKLTSVPKGLP 239  
 Db 173 NRIRKVPKGVFSLRNNMNCIEMGNPLENSGFQFAGFGLKLYLRISEAKLTGIPKDL 232  
 QY 240 PTLLEHLHDYNTSTVELEDFKRYKELORLGLGNKTTDIENGSLANIIPRVRIHLNNK 299  
 Db 233 ETLNELHLDHNDKQIAIELEDLRLYSKLYRGLGHNQIRMIENGSLSPFLTLRELHLDNNK 292  
 QY 300 LKIPSGLPPELKYLIIFLHNSIARVGNDFCPTVPKMKKSLYSALISLNNPVYKWEQ 359  
 Db 293 LSRVPAGLPDLKLVVLYHTNNTITKGVNDFCPVGVKRAYNGISLNNPVYWEQ 352  
 QY 360 PATFRCVLSRMSVOLGNF 377  
 Db 353 PATFRCVTDRLAIQFGNY 370

RESULT 8

PGSL\_SHEEP STANDARD; PRT; 369 AA.  
 AC 046390;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Biglycan precursor (Bone/cartilage proteoglycan I) (PG-SI).  
 GN BGN.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RC TISSUE=Choroid plexus;  
 RA Bruett L., Clements J.E.;  
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: May be involved in collagen fiber assembly (By similarity).  
 CC -!- SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).  
 CC -!- TISSUE SPECIFICITY: Found in several connective tissues, specially in articular cartilages.  
 CC -!- PTM: The two attached glycosaminoglycan chains can be either chondroitin sulfate or dermatan sulfate (By similarity).  
 CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN (SRP) FAMILY, CLASS I SUBFAMILY.  
 CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).  
 CC  
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 CC  
 CC EMBL; AF034842; AAB87988.1;  
 CC InterPro; IPR001611; LRR.  
 CC InterPro; IPR000372; LRR.Nterm.  
 CC InterPro; IPR003592; LRR.Out.  
 CC InterPro; IPR003591; LRR\_Typ.  
 CC Pfam; PF00560; LRR; 7.  
 CC Pfam; PF01462; LRRNT; 1.  
 CC SMART; SM00370; LRR; 3.  
 CC SMART; SM00013; LRRNT; 1.

DR SMART; SM00369; LRR\_Typ; 1.  
 KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;  
 Leucine-rich repeat; Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT PROPEP 20 37 BY SIMILARITY.  
 FT CHAIN 38 369 BIGLYCAN.  
 FT DOMAIN 64 77 CYS-RICH.  
 FT REPEAT 83 103 LRR-S 1.  
 FT REPEAT 104 127 LRR-T 1.  
 FT REPEAT 128 151 LRR-T 2.  
 FT REPEAT 152 172 LRR-S 2.  
 FT REPEAT 173 196 LRR-T 3.  
 FT REPEAT 197 221 LRR-T 4.  
 FT REPEAT 222 242 LRR-S 3.  
 FT REPEAT 243 266 LRR-T 5.  
 FT REPEAT 267 290 LRR-T 6.  
 FT REPEAT 291 313 LRR-S 4.  
 FT REPEAT 314 343 LRR-T 7.  
 FT REPEAT 344 369 LRR-T 8.  
 FT CARBOHYD 42 42 O-LINKED (GLYCOSAMINOGLYCAN) (BY SIMILARITY).  
 FT CARBOHYD 48 48 O-LINKED (GLYCOSAMINOGLYCAN) (BY SIMILARITY).  
 FT CARBOHYD 271 271 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 312 312 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT DISULFID 64 77 BY SIMILARITY.  
 FT DISULFID 322 355 BY SIMILARITY.  
 SQ SEQUENCE 369 AA; 41523 MW; 048C82C23390EE6 CRC64;  
 Query Match 51.6%; Score 1027.5; DB 1; Length 369;  
 Best Local Similarity 51.9%; Pred. No. 4.5e-64;  
 Matches 196; Conservative 67; Mismatches 96; Indels 19; Gaps 3;  
 QY 4 YVLLFLALCSAKPFSPSHIALKNMMLKMDTDDDD-----DDDDDDDDDDSLFPTR 59  
 Db 5 WLAALLALSOALPPEQ-----KAFWDFTLDDGLPMLNDEASGAETTSIGPDL 53  
 QY 60 EPRSHFFDFLPMCPFGCQCYRVVHCSDLGTSVPTNIPFDTRMLDQNNKIKEIKEN 119  
 Db 54 DS-----LPPTYSAMCPFGCHLRVVCQSDGLGKAVPKEISPDPTTLLDQNNISELRKD 109  
 QY 120 DFKGLTSLYGLIINNNKLTTHKPAFLTTKRLRLYLSHNOLSEIPLNLPKSLAEIRIHE 179  
 Db 110 DFKGLQHLVLYLVNNKISIKHEKAFSPLRKRLQKLYISKNLHVEIPNLPSSVLRLIHD 169  
 QY 180 NKVKIKQKDTFKGMALHVLSEMSANPLDNNNGIEPFAFEGVTVPFHRIAEAKLTSVPKGLP 239  
 Db 170 NRIRKVPKGVFSLRNNMNCIEMGNPLENSGFQFAGFGLKLYLRISEAKLTGIPKDL 229  
 QY 240 PTLLEHLHDYNTSTVELEDFKRYKELORLGLGNKTTDIENGSLANIIPRVRIHLNNK 299  
 Db 230 ETLNELHLDHNDKQIAIELEDLRLYSKLYRGLGHNQIRMIENGSLSPFLTLRELHLDNNK 289  
 QY 300 LKIPSGLPPELKYLIIFLHNSIARVGNDFCPTVPKMKKSLYSALISLNNPVYKWEQ 359  
 Db 290 LSRVPAGLPDLKLVVLYHTNNTITKGVNDFCPVGVKRAYNGISLNNPVYWEQ 349  
 QY 360 PATFRCVLSRMSVOLGNF 377  
 Db 350 PATFRCVTDRLAIQFGNY 367

RESULT 9

PGSL\_CANFA STANDARD; PRT; 369 AA.  
 AC 002678;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Biglycan precursor (Bone/cartilage proteoglycan I) (PG-SI).  
 GN BGN.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;









PGS2\_HUMAN STANDARD; PRT: 359 AA.  
 ID AC P07585; Q9Y5N9; Q9P0Z0; Q9P0Z1;  
 DT 01-APR-1988 (Rel. 07, Created)  
 DT 01-APR-1988 (Rel. 07, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Decorin precursor (Bone proteoglycan II) (PG-S2) (PG40).  
 GN DCN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RN R1 MEDLINE=87017013; PubMed=3484330;  
 RA Krusius T., Ruoslahti E.;  
 RP "Primary structure of an extracellular matrix proteoglycan core  
 RT protein deduced from cloned cDNA";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:7683-7687(1986).  
 [2]  
 RN R2 MEDLINE=93162643; PubMed=8432527;  
 RA Vetter U., Vogel W., Just W., Young M.F., Fisher L.W.;  
 RP "Human decorin gene: Intron-exon junctions and chromosomal  
 RT localization";  
 RL Genomics 15:161-168(1993).  
 [3]  
 RN R3 MEDLINE=93162642; PubMed=8432526;  
 RA Danielson K.G., Fazio A., Cohen I.R., Cannizzaro L., Iozzo R.V.;  
 RP "The human decorin gene: Intron-exon organization, discovery of two  
 RT alternatively spliced exons in the 5' untranslated region, and  
 RL mapping of the gene to chromosome 12q23.";  
 [4]  
 RN R4 Cs-Szabo G., Gant T.T.;  
 RP "Alternative splicing of human decorin.";  
 RT Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 [5]  
 RN R5 SEQUENCE FROM N.A.  
 RP TISSUE=Liver;  
 RA Strausberg R.;  
 RP Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 [6]  
 RN R6 MEDLINE=90073579; PubMed=2590169;  
 RA Roughley P.J., White R.J.;  
 RP "Dermatan sulphate proteoglycans of human articular cartilage. The  
 RT properties of dermatan sulphate proteoglycans I and II";  
 RL Biochem. J. 262:823-827(1989).  
 [7]  
 RN R7 MEDLINE=87250639; PubMed=3597437;  
 RA Fisher L.W., Hawkins G.R., Tuross N., Termine J.D.;  
 RP "Purification and partial characterization of small proteoglycans I  
 RT and II, bone sialoproteins I and II, and osteonectin from the mineral  
 CC compartment of developing human bone.";  
 CC J. Biol. Chem. 262:9702-9708(1987).  
 CC -!- FUNCTION: May affect the rate of fibrils formation.  
 CC -!- SUBUNIT: Binds to type I and type II collagen, to fibronectin and  
 CC TGF-beta. Forms a ternary complex with MFAP2 and ELN (by  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Extracellular matrix.  
 CC -!- ALTERNATIVE PRODUCTS: 5 isoforms; A (shown here), B, C, D and E;  
 CC are produced by alternative splicing.  
 CC -!- PTM: The attached glycosaminoglycan chain can be either  
 CC chondroitin sulfate or dermatan sulfate depending upon the tissue  
 CC of origin.  
 CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS  
 CC (SLRPS) FAMILY. CLASS I SUBFAMILY.  
 CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).  
 CC  
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 CC  
 CC EMBL: M14219; AA800774.1; -;  
 CC EMBL: L01131; AA52301.1; ALT\_SEQ.  
 CC EMBL: L01125; AA52301.1; JOINED.  
 CC EMBL: L01126; AA52301.1; JOINED.  
 CC EMBL: L01127; AA52301.1; JOINED.  
 CC EMBL: L01129; AA52301.1; JOINED.  
 CC EMBL: L01130; AA52301.1; JOINED.  
 CC EMBL: M98262; AAB60901.1; -;  
 CC EMBL: AF138300; AAD4713.1; -;  
 CC EMBL: AF138301; AAF61437.1; -;  
 CC EMBL: AF138302; AAD44714.1; -;  
 CC EMBL: AF138303; AAF61438.1; -;  
 CC EMBL: AF138304; AAD44715.1; -;  
 CC EMBL: BC005322; AAH05322.1; -;  
 CC PIR: A26476; NBHUC8.  
 CC PIR: S05640; S05640.  
 CC PIR: B28457; B28457.  
 CC PIR: A45016; A45016.  
 CC Genew; HGNC:2705; DCN.  
 CC MIM: 125255; -;  
 CC InterPro: IPR001611; LRR.  
 CC InterPro: IPR000372; LRR Nterm.  
 CC InterPro: IPR003592; LRR out.  
 CC InterPro: IPR003591; LRR typ.  
 CC Pfam: PF00560; LRR; 7.  
 CC Pfam: PF01462; LRRNT; 1.  
 CC SMART; SM00370; LRR; 3.  
 CC SMART; SM00013; LRRNT; 1.  
 CC SMART; SM00369; LRR\_TYP; 1.  
 CC Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;  
 CC Leucine-rich repeat; Signal; Alternative splicing; Polymorphism.  
 CC  
 CC SIGNAL 1 16  
 CC FT PROPEP 17 30  
 CC FT CHAIN 31 359  
 CC FT DOMAIN 54 67  
 CC FT REPEAT 73 93  
 CC FT REPEAT 94 117  
 CC FT REPEAT 118 141  
 CC FT REPEAT 142 162  
 CC FT REPEAT 163 186  
 CC FT REPEAT 187 212  
 CC FT REPEAT 213 233  
 CC FT REPEAT 234 257  
 CC FT REPEAT 258 281  
 CC FT REPEAT 282 304  
 CC FT REPEAT 305 334  
 CC FT REPEAT 335 359  
 CC FT DISULFID 34 67  
 CC FT DISULFID 313 346  
 CC FT CARBOHYD 34 34  
 CC FT CARBOHYD 211 211  
 CC FT CARBOHYD 262 262  
 CC FT CARBOHYD 303 303  
 CC FT VARSPLIC 71 179  
 CC FT VARSPLIC 73 219  
 CC FT VARSPLIC 109 295  
 CC FT VARSPLIC 172 75  
 CC FT VARSPLIC 76 359  
 CC FT VARIANT 273 273  
 CC FT CONFLICT 37 37  
 CC FT CONFLICT 45 45  
 CC SEQUENCE 359 AA; 39746 MW; FF511B871A1A52DD CRC64;





FT	PROPEP	17	30
FT	CHAIN	31	360
FT	DOMAIN	55	68
FT	REPEAT	74	94
FT	REPEAT	95	118
FT	REPEAT	119	142
FT	REPEAT	143	163
FT	REPEAT	164	187
FT	REPEAT	188	213
FT	REPEAT	214	234
FT	REPEAT	235	258
FT	REPEAT	259	282
FT	REPEAT	283	305
FT	REPEAT	306	335
FT	REPEAT	336	360
FT	DISULFID	55	68
FT	DISULFID	314	347
FT	CARBOHYD	34	34
FT			
FT	CARBOHYD	212	212
FT	CARBOHYD	263	263
FT	CARBOHYD	304	304
FT	SEQUENCE	360 AA;	39837 MW; 71E84DA2B87552C0 CRC64;
SQ			
	Query Match	47.3%;	Score 943; DB 1; Length 360;
	Best Local Similarity	49.1%;	Pred. No. 3e-58;
	Matches 186;	Conservative 69;	Mismatches 102; Indels 22; Gaps
QY	1 MKEYVLLFLALCS-AKPFSPSHIALKNMMLKDMETDDDDDDDDDDDEDNSLPFTR	59	
Db	1 MKATITPFLVAQSWAGPF---QQKGIFDFPL-----EDEASGIGPEEHFPEVPEI	48	
QY	60 EPRSHFFPDFLPMCPGCCYCYSRVVHCSDLGTSVPTNIPFDTRLMDLQNNKIKEIKEN	119	
Db	49 EP-----MGVPVPCRCOCHLRVWCDSGLGEKVPKDLPPDTALLDQNNKITKDQ	100	
QY	120 DFKGLTSLYLILNNKLTKIHPEKAFTTTKKRLRLLSHNQLSSEIPLNLPSKLAELRIHE	179	
Db	101 DFNKLNLHTLILNNKISKISPGAFAPLVKLERLYSKNQLKELPEKMPKTLOELRVHE	160	
QY	180 NKVKKIOKDTFGKMNALHVLMSANPLDNNGIEPGAEGV-TVPHIRIAEAKLTSPVKGL	238	
Db	161 NEITKVRKSVFNLGNQMIVVELGTNPCLKSSGIENGAFQGMMKLSYRIADNTTIPOGL	220	
QY	239 PPTLEHLHDYNKSTVELEDKFYKRELQRLGLGNKKITTDIENGSLANTIPRVREIHLENN	298	
Db	221 PPSLTELHLGDGNIKTVDAAASLGLNNAKLGLSFSNISAVDNGSLANTPHLRELHNNA	280	
QY	299 KKKIPSGLPKELYQTIIFLHSNISARVGVNDFCPTVPKMKKLSYSAISLFNNPVKYWEM	358	
Db	281 KLAKVPGVADHKYIQVVYLHNNNISAGSNDFCCPGYNTKKASYGSVSLSFPVQYWEI	340	
QY	359 QPATFRCVLSRMVSQJGNF	377	
Db	341 QPSTFRVCVYVRAAVALGNV	359	
	RESULT 17		
ID	PGS2_RABIT	STANDARD;	PRT; 360 AA.
AC	Q28608;		
DT	15-JUL-1999 (Rel. 38, Created)		
DT	15-JUL-1999 (Rel. 38, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Decorin precursor (Bone proteoglycan II) (PG-S2).		
GN	DCN.		
OS	Oryctolagus cuniculus (Rabbit).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OX	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.		
NCBI_TaxId	9986;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Gorrea;		

```

RX MEDLINE=95122319; PubMed=7822148;
RA Zhan Q., Burrows R., Cinton C.;
RT "Cloning and in situ hybridization of rabbit decorin in corneal
RL tissues.";
RN Invest. Ophthalmol. Vis. Sci. 36:206-215(1995).
[2]
RP SEQUENCE OF 38-358 FROM N.A.
RC TISSUE=Cartilage;
RA Hering T.M., Kollar J.;
RT "The primary structure of rabbit chondrocyte decorin deduced from
RL nucleotide sequence.";
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May affect the rate of fibrils formation (By
CC similarity).
CC -!- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
CC TGF-beta. Forms a ternary complex with MFAP2 and ELN (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
CC -!- PTM: The attached glycosaminoglycan chain can be either
CC chondroitin sulfate or dermatan sulfate depending upon the tissue
CC of origin (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
CC (SLRPS) FAMILY. CLASS I SUBFAMILY
CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
CC
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CC
DR EMBL: S76584; AAC33083.1; -
DR EMBL: U03394; AAC04315.1; -
DR InterPro: IPR001611; LRR.
DR InterPro: IPR003372; LRR_Nterm.
DR InterPro: IPR003592; LRR_Out.
DR InterPro: IPR003591; LRR_Typ.
DR Pfam: PF00560; LRR_7.
DR Pfam: PF01462; LRRNT; 1.
DR SMART: SM00370; LRR; 1.
DR SMART: SM00013; LRRNT; 1.
DR SMART: SM00369; LRR_Typ; 1.
DR Glycoprotein: Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal.
FT SIGNAL 1 16
FT PROPEP 17 30
FT CHAIN 31 360
FT DOMAIN 55 68
FT REPEAT 74 94
FT REPEAT 95 118
FT REPEAT 119 142
FT REPEAT 143 163
FT REPEAT 164 187
FT REPEAT 188 213
FT REPEAT 214 234
FT REPEAT 235 258
FT REPEAT 259 282
FT REPEAT 283 305
FT REPEAT 306 335
FT REPEAT 336 360
FT REPEAT 314 347
FT DISULFID 55 68
FT DISULFID 314 347
FT CARBOHYD 34
FT
FT CARBOHYD 212 212
FT CARBOHYD 263 263
FT CARBOHYD 304 304
FT CARBOHYD 360 AA; 39896 MW; OB50C6756FE02369 CRC64;
SQ SEQUENCE 360 AA; 47.2%; Score 941; DB 1; Length 360;
Query Match 47.2%; Score 941; DB 1; Length 360;
Best Local Similarity 49.6%; Pred. No. 4.le-58;

```

## RESULT 18

```

PGS2_HORSE
ID PGS2_HORSE STANDARD; PRT; 360 AA.
AC 046542;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Decorin precursor (Bone proteoglycan II) (PG-S2) (Dermatan sulfate
DE proteoglycan II) (DS-PGII).
GN DCN
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Richardson D.W., Dodge G.R.;
RT "Effects of interleukin-1 beta and tumor necrosis factor-alpha on the
RT expression of matrix related genes in cultured equine articular
RT chondrocytes.";
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May affect the rate of fibrils formation (By
CC similarity).
CC -!- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
CC TGF-beta. Forms a ternary complex with MFAP2 and ELN (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
CC -!- PTM: The attached glycosaminoglycan chain can be either
CC chondroitin sulfate or dermatan sulfate depending upon the tissue
CC of origin (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
CC (SLRPS) FAMILY. CLASS I SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
CC
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CC

```

```

Matches 188; Conservative 67; Mismatches 102; Indels 22; Gaps 5;
Qy 1 MKEVLLIFALCS-AKPFSPSHALKNMMLKDMEDTDDDDDDDDDDDDDDDDNSLEPTR 59
Db 1 MTATLILLLLAQSAGGPF---QQRGLDFMLED-EASGIGPDERAPELPDLDM----- 50
Qy 60 EPRSHFPFDLFPMPFCQCYSRVVHCSDLGLTSVPTNIPFDTRMIDLQNNKIKEIKEN 119
Db 51 -----LGPVCFRCQCHLRVQCSDLGLQKPKDLPDPDTLLDLQNNKITEIKDG 100
Qy 120 DFKGLTSLYGLILNNKLTIKHPKAFLLTKLRRLYLSSHQSLSEIPLNLPKSLAELRIHE 179
Db 101 DFKNLNLHALILYNNKISKISPGAFPLVKRLRLYSKLNHLKELPEKMPKSLQELRAHE 160
Qy 180 NKVKIKQKDTFKGMNALHVMESANPLDNNNGIEPGAGEV-TVPHIRIAEAKLTSPVKGL 238
Db 161 NEITKVRKSVFSGMNMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADNITITPQGL 220
Qy 239 PPTLELHLDYNNKISTVELEDFKRYKELQRLGNGNKTIDENGSLANIPIVRREIHLNEN 298
Db 221 PPSLTLEHLDGNKITKIDASSLKGILNNLAKLGLSFNDISAVDNGSLANAPHLRELHLDN 280
Qy 299 KLKIPSGLPKLYLOIIFLHNSIARVGVNDFCTVPKMKKSLYSALSIFNNPKYKWM 358
Db 281 KLIRVPGGLDHKTIQVYLLNNLSVVGANDFCPPGYNTKKASYSGVSLFSNPVQWEI 340
Qy 359 QPATFRCVLSRMSVQLGNF 377
Db 341 QPSTFRCVYMRSAIQLGNY 359

```



```

CC      (SLRPS) FAMILY, CLASS I SUBFAMILY.
CC      -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
CC      -----
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CC      -----
DR      EMBL; X53929; CAA37876.1; -.
DR      PIR; S20812; S20812.
DR      HSSP; P23945; LXUN.
DR      MGD; MGI:94872; Dcn.
DR      InterPro; IPR001611; LRR.
DR      InterPro; IPR000372; LRR_Nterm.
DR      InterPro; IPR003592; LRR_Out.
DR      InterPro; IPR003591; LRR_typ.
DR      Pfam; PF00560; LRR; 9
DR      Pfam; PF01462; LRRNT; 1.
DR      SMART; SM00370; LRR; 2.
DR      SMART; SM00013; LRRT; 1.
DR      SMART; SM00369; LRR_TYP; 2.
KW      Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW      Leucine-rich repeat; Signal.
FT      SIGNAL          1..16   POTENTIAL.
FT      PROPEP         17..30
FT      CHAIN          31..354
FT      DOMAIN         49..62
FT      REPEAT         68..88
FT      REPEAT         89..112
FT      REPEAT        113..136
FT      REPEAT        137..157
FT      REPEAT        158..181
FT      REPEAT        182..207
FT      REPEAT        208..231
FT      REPEAT        229..252
FT      REPEAT        253..276
FT      REPEAT        277..299
FT      REPEAT        300..329
FT      REPEAT        330..354
FT      DISULFID       49..62
FT      DISULFID      308..341
FT      CARBOHYD       34..34
FT      FT             206
FT      FT             241
FT      FT             241
FT      FT             257
FT      FT             298
SQ      SEQUENCE       354 AA; 39809 MW; F05B5CC08DCABF6F CRC64;
Query Match           45.6%; Score 907.5; DB 1; Length 354;
Best Local Similarity 52.0%; Pred. No. 8,3e-56;
Matches 170; Conservative 65; Mismatches 87; Indels 5; Gaps 2;
QY      56 FPTREKSHFPFED-----LFPMCFPGQCYSRVVHCSDGLGTSVTPIPFOTRMLDQNN 111
Db      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      27 FMLEDEASGITIPDPDNPLISMCPYRCQCHLVVVQCSDGLGDKVPWFPPDTTLILDQNN 86
Db      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      112 KIKEIKENDFKGLTSLYLINLNKLTIHPKAPLTTKLRRLYLSHNSOLSEIPLNPKS 171
Db      | | | | | | | | | : | : | : | : | : | : | : | : | : | : | : | : |
QY      87 KITEIKEGAFKNLDLHTLIIVNNKISKISPEAKPLVKLERLYSNQLKELPEKPAPT 146
Db      | | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      172 LAELRIHENKKVKTOKDTFKGMNALHVLEMSANPDNNGIEPGAPEGV-TVFHIRIAEK 230
Db      | | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      147 LQELRVHENEITLKRSDFENGNNVLVELGGNPLKNSGIENGAFQGLKLSLYTRISDTN 206
Db      | | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      231 LTSVPKGLPLTLEHLHDYNKISTIVELEDKRYKELORLGLGNKKKITDIENGSIANIPRV 290
Db      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      207 ITAIPOGLQTSLTEVHLDGNNKITKVDAPSLLKLNLSKLGIFSNIWMENGSIANNPHL 266
Db      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      291 REIHLNENKLIKTPSGLPPELKLIQIFIELHSNSTARVGWDFCPTVPVRMKKSLEYSAISLFN 350

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Db 267 RELHLDNNKLLRVPAGLAHQYIQVYLLHNNNISAVGONDFCRAGHSRKRASYSAVSLYG 326
QY 351 NPVKWEMQATFRCVLSRMSVOLGNF 377
Db 327 NPVRYWEIFPNTFCVYVRSATQLGNY 353

RESULT 21
PGS2_RAT
ID PGS2_RAT STANDARD; PRU; 354 AA.
AC Q01129;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Decorin precursor (Bone proteoglycan II) (PG-S2) (PG40) (Dermatan
GN sulfate proteoglycan-II) (DSPE).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Uterus;
RX MEDLINE=93003331; PubMed=1390895;
RA Abramson S.R.; Woessner J.F.;
RT "cDNA sequence for rat dermatan sulfate proteoglycan-II (decorin).";
RL Biochim. Biophys. Acta 1132:225-227(1992).
RN [2]
SEQUENCE OF 11-354 FROM N.A.
RX MEDLINE=93154359; PubMed=1493796;
RA Asundi V.K.; Dreher K.L.;
RT "Molecular characterization of vascular smooth muscle decorin;
RT deduced core protein structure and regulation of gene expression.";
RL Eur. J. Cell Biol. 59:314-321(1992).
RN [3]
SEQUENCE OF 31-48 AND 171-191.
RC STRAIN=Sprague-Dawley; TISSUE=Uterus;
RX MEDLINE=89350825; PubMed=2764879;
RA Kokenyesi R.; Woessner J.F.;
RT "Purification and characterization of a small dermatan sulphate
RT proteoglycan implicated in the dilatation of the rat uterine
RT cervix.";
RL Biochem. J. 260:413-419(1989).
CC -!- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
CC -!- FUNCTION: May affect the rate of fibrils formation (By
CC similarity). May be implicated in the dilatation of the rat
CC cervix.
CC -!- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
CC -!- FUNCTION: Forms a ternary complex with MFAP2 and ELN (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular matrix.
CC -!- DEVELOPMENTAL STAGE: The amount of DSPG per cervix increases 4-
CC fold during pregnancy, then falls precipitously within 1 day post
CC partum.
CC -!- PM: The attached glycosaminoglycan chain can be either
CC chondroitin sulfate or dermatan sulfate depending upon the tissue
CC of origin (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
CC (SERPS) FAMILY. CLASS I SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: Z12298; CAA78170.1; -.
CC EMBL: X59659; CAA42519.1; -.
CC PIR: S29145; S29145.

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DR InterPro: IPR001611; LRR.
DR InterPro: IPR003372; LRR_Nterm.
DR InterPro: IPR003592; LRR_Out.
DR InterPro: IPR003591; LRR_typ.
DR Pfam: PF00560; LRR: 8.
DR Pfam: PF01462; LRRNT: 1.
DR SMART: SM00370; LRR: 2.
DR SMART: SM00013; LRRNT: 1.
DR SMART: SM00369; LRR_typ: 2.
KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT PROPEP 17 30
FT CHAIN 31 354 DECORIN.
FT DOMAIN 49 62
FT REPEAT 68 88 LRR-S 1.
FT REPEAT 89 112 LRR-T 1.
FT REPEAT 113 136 LRR-T 2.
FT REPEAT 137 157 LRR-S 2.
FT REPEAT 158 181 LRR-T 3.
FT REPEAT 182 207 LRR-T 4.
FT REPEAT 208 228 LRR-S 3.
FT REPEAT 229 252 LRR-T 5.
FT REPEAT 253 276 LRR-T 6.
FT REPEAT 277 299 LRR-S 4.
FT REPEAT 300 329 LRR-T 7.
FT REPEAT 330 354 LRR-T 8.
FT DISULFID 49 62 BY SIMILARITY.
FT DISULFID 308 341 O-LINKED (GLYCOSAMINOGLYCAN) (BY
FT CARBOHYD 34 34 SIMILARITY).
FT CARBOHYD 184 184 O-LINKED (GLYCOSAMINOGLYCAN) (BY
FT CARBOHYD 206 206 SIMILARITY).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 257 257 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 298 298 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 354 AA; 39805 MW; 152D92F42D9F5A5B CRC64;

Query Match 45.1%; Score 899; DB 1; Length 354;
Best Local Similarity 46.5%; Pred. No. 3.2e-55;
Matches 178; Conservative 70; Mismatches 99; Indels 36; Gaps 5;

QY 1 MKEYVLLFLALCS-AKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDDDDDD 59
Db 1 MKATLVFLLAQVSWAGPF---EQRGLDFMLEDDDDDDDDDDDDDDDDDDDDDDDD 31
QY 60 EPRSHEFFPD----LPPMCPFGCQCYSRVHCGSDGLTSVPTNIPDTRMLDLQNNKIKE 115
Db 32 -EASGIIPYDPDNPLISMCPYRCQCHLRVVQCSGLGDKVPWFEPDPTLLDLQNNKITE 90
QY 116 IKENDPKGLTSLYGLILNNKLTTHKPKAFLLTKLRLRLYLSHNSLSEIPLNPKSLAEL 175
Db 91 IKEGAFKPKLDLHTLLVNNKISKISPEAFKPLVLRLYLSKNHLKELPKLPTLQEL 150
QY 176 RIHENVKKTKQDKTFKGMNALHVLMSANPLDNGIEPCAFEGVT-VFHIRIAEAKLTSV 234
Db 151 RUHNDNITKLLKSVFNGLMRIVIEIGNPLKNSGIEGALQGMKGLGIRISDNITAI 210
QY 235 PKGLPPTLLEHLHDYKNISTVELEDFKRYKELQRLGLGNKKTIDTENGSLANIPRVREH 294
Db 211 PQGLPSTISELHLDGNKIADVAASLKGNLSKGLSFNSITVVGSLANVPHLREH 270
QY 295 LNNKLUKTPSGLPDELKYLQITFLHSNSTARVGVNDPCTVPKMKKLSYSAISLNNPVK 354
Db 271 LDNNKLLRYPAGLAHQYIQVYVLLHNNNISAVGONDFCRLPSYQTRKTSYAVSLYSNPVR 330
QY 355 YWEMQATFRCVLSRMSVOLGNF 377
Db 331 YWOIHPHTFRCVFGSRSTIQLGNY 353

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RESULT 22

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PGS1_PIG
ID PGS1_PIG STANDARD; PRT; 272 AA.
AC O9K06: Q9TTB5;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Biglycan precursor (Bone/cartilage proteoglycan I) (PG-S1)
DE (Fragments).
GN BGN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP TISSUE=Aorta;
RC TISSUE=Heart;
RA Zhao B.;
RA Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP TISSUE=Skin;
RC TISSUE=Skin;
RA Wang J.F., Boykiw R.H., Reno C.R., Olson M.E., Hart D.A.;
RT "Cloning and sequencing of porcine matrix molecules.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May be involved in collagen fiber assembly (By
CC similarity).
CC -!- SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
CC -!- TISSUE SPECIFICITY: Found in several connective tissues, specially
CC in articular cartilages.
CC -!- PTM: The two attached glycosaminoglycan chains can be either
CC chondroitin sulfate or dermatan sulfate (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
CC (SLRPS) FAMILY. CLASS I SUBFAMILY.
CC -!- SIMILARITY: CONTAINS AT LEAST 9 LEUCINE-RICH REPEATS (LRR).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF054419; AAC39274.1; -
DR EMBL; AF159382; AAF19153.1; -
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF01462; LRRNT; 1.
DR Pfam; PF00560; LRR; 4.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_Typ; 1.
DR Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; signal.
FT SIGNAL 1 19
FT PROPEP 20 37 BY SIMILARITY.
FT CHAIN 38 272 BIGLYCAN.
FT DOMAIN 64 77 CYS-RICH.
FT REPEAT 83 103 LRR-S 1.
FT REPEAT 104 127 LRR-T 1.
FT REPEAT 128 >137 LRR-T 2.
FT NON_CONS 137 138
FT REPEAT <138 152
FT REPEAT 153 173 LRR-S 3.
FT REPEAT 174 197 LRR-T 5.
FT REPEAT 198 221 LRR-T 6.
FT REPEAT 222 244 LRR-S 4.
FT REPEAT 245 >272 LRR-T 7.
FT CARBOHYD O-LINKED (GLYCOSAMINOGLYCAN) (BY
FT SIMILARITY).
FT CARBOHYD O-LINKED (GLYCOSAMINOGLYCAN) (BY

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FT DISULFID 64 77 SIMILARITY).
FT NON_TER 272 BY SIMILARITY.
SQ SEQUENCE 272 AA; 30457 MW; 6EBBAD0EF86378BB CRC64;

Query Match 32.28; Score 641; DB 1; Length 272;
Best Local Similarity 39.18; Pred. No. 1.5e-37;
Matches 138; Conservative 52; Mismatches 73; Indels 90; Gaps 5;

QY 4 YVLLIFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDD-----DDDDDDDDDDSDSLFPT 58
DB 5 WLLASLLALSQALPEQ-----KAFWDFTLDDGLPLMNDERASGADSTGSI--- 50
QY 59 RPSRSHFPFDLFPMPGFCOCYRVVHCSDLGTSVPTNPFTPTMLDLDONNKIKEKE 118
DB 51 --PDLDALPPTFTSAMCPFGCHLRVVCQSLGKAVKPEISPDPTLLDQNNDISLRK 108
QY 119 NDFKGLTSYGLIILNNKLTHTKPKAFITTKLRLRLYLHSHNLSEIPLNLPKSLAELRIH 178
DB 109 DDFKGLHLYALVLVNNKISR-----STR----- 133
QY 179 ENKVKKIQKDTFKGMNALHVLMSANPLDNGIEGAFEGVTVPFHRIAIAEAKLTSVPKGL 238
DB 134 -----PSAPDGLKLVLRISAEAKLTGPKDL 159
QY 239 PPTLELHLDYNKISTVEDEPKRYKELQRLGLGNKKTIDIEGSLANIPRVREIHLENN 298
DB 160 PETLNELDHDKIOAIELELLRYSKLYRLGLGHQNRMIENGSLSFPLTRLEHLDNN 219
QY 299 KKKKTPSGPELKYLIITFLHNSIARVGNDFCPTVPKMKKSLYSATSLFNN 351
DB 220 KLSRVFAGLPDLKLQVYLLTNNTKVGVDNFCVGFVGRAYNGISLNN 272

RESULT 23
PGS1_RABIT
ID PGS1_RABIT STANDARD; PRT; 135 AA.
AC O46377;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Biglycan (Bone/cartilage proteoglycan I) (PG-S1) (Fragment).
GN BGN.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand white;
RX MEDLINE=99037997; PubMed=9822203;
RA Boykiw R.H., Sciore P., Reno C.R., Marchuk L., Frank C., Hart D.A.;
RT "Altered levels of extracellular matrix molecules mRNA in healing
RT rabbit ligaments.";
RL Matrix Biol. 171:371-378(1998).
CC -!- FUNCTION: May be involved in collagen fiber assembly (By
CC similarity).
CC -!- SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
CC -!- TISSUE SPECIFICITY: Found in several connective tissues, specially
CC in articular cartilages.
CC -!- PTM: The two attached glycosaminoglycan chains can be either
CC chondroitin sulfate or dermatan sulfate (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
CC (SLRPS) FAMILY. CLASS I SUBFAMILY.
CC -!- SIMILARITY: CONTAINS AT LEAST 6 LEUCINE-RICH REPEATS (LRR).
CC -----
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EMBL: AF020290; AAC39515.1; -

InterPro: IPR001611; LRR.

InterPro: IPR003591; LRR\_Typ.

SMART: SM00369; LRR; 5.

SMART: SM00369; LRR\_Typ; 1.

Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;

Leucine-rich repeat.

NON\_TER 1

REPEAT <1 15 LRR-T 4.

REPEAT 16 36 LRR-S 3.

REPEAT 37 60 LRR-T 5.

REPEAT 61 84 LRR-T 6.

REPEAT 85 107 LRR-S 4.

REPEAT 108 >135 LRR-T 7.

NON\_TER 135 135

SEQUENCE 135 AA; 15323 MW; EFDC6E74D42F5098 CRC64;

Query Match 22.2%; Score 442; DB 1; Length 135;

Best Local Similarity 59.3%; Pred. No. 3.5e-24;

Matches 80; Conservative 30; Mismatches 25; Indels 0; Gaps 0;

Qy 217 EGVTVFHRIAEAKLTSVPGKLPPTLLEHLHDYDKISTVELEDFKRYKELQRLGLGNKI 276

Db 1 DGLKINYLRISSEKLTGIPRODLPETLNLHLDHKNKIOAIELEDLRLSKYRLGLGNQI 60

Qy 277 TDINGSANIPRVREIHLNENKLIKPSGLPELKYQLIIFLHNSNISTARVGNDFCPTVP 336

Db 61 RMIENGSLSELPTRRELHLDNKNLSRVAGLPDLKLQVVLHNSNITKVGNDFCVGF 120

Qy 337 KMKKSLYSALSLENN 351

Db 121 GVKRAYNGISLENN 135

RESULT 24

LUM\_CHICK STANDARD; PRT; 343 AA.

AC P51890;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Lumican precursor (Keratan sulfate proteoglycan lumican) (KSPG

DE Lumican).

GN LUM OR LDC.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OC NCBI\_TaxID=9031;

OX [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=92112674; PubMed=1370446;

RX Blochberger T.C., Vergnes J.-P., Hempel J., Hassell J.R.;

RT "cDNA to chick lumican (corneal keratan sulfate proteoglycan) reveals

RT homology to the small interstitial proteoglycan gene family and

RL expression in muscle and intestine."

RL J. Biol. Chem. 267:347-352(1992).

RN [2]

RP SEQUENCE OF 79-85; 155-167 AND 246-256, AND CARBOHYDRATE-LINKAGE SITES

RP ASN-91; ASN-165 AND ASN-257.

RC TISSUE=Cornea;

RA MEDLINE=98211990; PubMed=9545293;

RX Dunley J.R., Neame P.J., Vergnes J.-P., Hassell J.R.;

RT "Identification of the N-linked oligosaccharide sites in chick corneal

RT lumican and keratan that receive keratan sulfate."

RL J. Biol. Chem. 273:9615-9621(1998).

CC -!- SUBUNIT: Binds to laminin (By similarity).

CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).

CC -!- TISSUE SPECIFICITY: Cornea and other tissues.

CC -!- PFM: Binds keratan sulfate chains.

-----

EMBL: AF020290; AAC39515.1; -

InterPro: IPR001611; LRR.

InterPro: IPR003591; LRR\_Typ.

SMART: SM00369; LRR; 5.

SMART: SM00369; LRR\_Typ; 1.

Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;

Leucine-rich repeat.

NON\_TER 1

REPEAT <1 15 LRR-T 4.

REPEAT 16 36 LRR-S 3.

REPEAT 37 60 LRR-T 5.

REPEAT 61 84 LRR-T 6.

REPEAT 85 107 LRR-S 4.

REPEAT 108 >135 LRR-T 7.

NON\_TER 135 135

SEQUENCE 135 AA; 15323 MW; EFDC6E74D42F5098 CRC64;

Query Match 20.1%; Score 399.5; DB 1; Length 343;

Best Local Similarity 31.9%; Pred. No. 9.6e-21;

Matches 104; Conservative 72; Mismatches 125; Indels 25; Gaps 9;

Qy 67 PEDLPMPCPFG-----CQC-----YSRVVHCSDLGTSVPTNPEDFMRDLQNNKIK 114

Db 24 PADDYDYPFGSTAVCAPECNCPISYPTAMVCDNLKLTPI-VPSGKIKYILRNMMIE 82

Qy 115 ETKENDFKGLTSLYGLILNNKL--TKIHPKAPLTTKLRLRLYLHSHQNSEIPLNPKSL 172

Db 83 ATEENTFDNVTDLQWLIDHNLHLENSKIKGRVFSKLNKLKLNHNNLTAVGPLPKTL 142

Qy 173 AELRTHENKVKLQKDTFKGMALHVLNANPLDNGIEPGAFGV-TVFHRTAEAKL 231

Db 143 DLQLSHNKITKVNPGALEGLVNLTVIHLQNNQLKTDNIS-GAFKGLNLLYLDLSFNOL 201

Qy 232 TSPVKGLPTLLEHLDYDKISTVELEDFKRYKELQRLGLGNKKTIDIE-NGSLANIPRV 290

Db 202 TKLPTGLPHSLMLYFDNNQISNIPDEYFGQFKTQYLRSLHINKLTDSDIPGVNFTISL 261

Qy 291 REIHLNENKLIKPSGLPELK--YLQIIFLHNSNISTARVGNDFCPTVPKMKKSLYSALS 348

Db 262 VELDLSENLQKSIPTVSENLENFYLQV-----NKNKPLSLSFCKVVGPLTYSKITHRL 316

Qy 173 AELRTHENKVKLQKDTFKGMALHVLNANPLDNGIEPGAFGV-TVFHRTAEAKL 231

Db 143 DLQLSHNKITKVNPGALEGLVNLTVIHLQNNQLKTDNIS-GAFKGLNLLYLDLSFNOL 201

Qy 232 TSPVKGLPTLLEHLDYDKISTVELEDFKRYKELQRLGLGNKKTIDIE-NGSLANIPRV 290

Db 202 TKLPTGLPHSLMLYFDNNQISNIPDEYFGQFKTQYLRSLHINKLTDSDIPGVNFTISL 261

Qy 291 REIHLNENKLIKPSGLPELK--YLQIIFLHNSNISTARVGNDFCPTVPKMKKSLYSALS 348

Db 262 VELDLSENLQKSIPTVSENLENFYLQV-----NKNKPLSLSFCKVVGPLTYSKITHRL 316

Qy 173 AELRTHENKVKLQKDTFKGMALHVLNANPLDNGIEPGAFGV-TVFHRTAEAKL 231

Db 143 DLQLSHNKITKVNPGALEGLVNLTVIHLQNNQLKTDNIS-GAFKGLNLLYLDLSFNOL 201

Qy 232 TSPVKGLPTLLEHLDYDKISTVELEDFKRYKELQRLGLGNKKTIDIE-NGSLANIPRV 290

Db 202 TKLPTGLPHSLMLYFDNNQISNIPDEYFGQFKTQYLRSLHINKLTDSDIPGVNFTISL 261

Qy 291 REIHLNENKLIKPSGLPELK--YLQIIFLHNSNISTARVGNDFCPTVPKMKKSLYSALS 348

Db 262 VELDLSENLQKSIPTVSENLENFYLQV-----NKNKPLSLSFCKVVGPLTYSKITHRL 316

QY 349 FNNPVKYMOPATFRVCVLSRMSVOL 374  
 Db 317 DGNLTRLADLPQEMYNCLRVAADISL 342

RESULT 25  
 LUM\_COTJA STANDARD; PRT; 343 AA.

AC Q9DE67;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lumican precursor (Keratan sulfate proteoglycan lumican) (KSPG lumican).  
 DE LUM OR LDC.  
 GN Coturnix coturnix japonica (Japanese quail).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;  
 OC Coturnix.  
 OX NCBI\_TaxID=93934;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Cornea;  
 RX MEDLINE=20556471; PubMed=11102759;  
 RA Corpuz L.M., Dunlevy J.R., Hassell J.R., Conrad A.H., Conrad G.W.;  
 RT "Molecular cloning and relative tissue expression of decorin and  
 lumican in embryonic quail cornea."  
 RL Matrix Biol. 19:699-704(2000).  
 CC -1- SUBUNIT: Binds to laminin (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).  
 CC -1- PTM: Binds keratan sulfate chains (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS  
 (SLRPS) FAMILY. CLASS II SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).  
 CC -----  
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: AF125251; AAC48155.1; -;  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR003372; LRR\_Nterm.  
 DR InterPro: IPR003592; LRR\_Out.  
 DR InterPro: IPR003591; LRR\_typ.  
 DR Pfam: PF00560; LRR; 9.  
 DR Pfam: PF01462; LRRNT; 1.  
 DR PRINTS: PR00019; LEURICHRPT.  
 DR SMART: SM00370; LRR; 4.  
 DR SMART: SM00013; LRRNT; 1.  
 DR SMART: SM00369; LRR\_TYP; 8.  
 DR Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;  
 KW Leucine-rich repeat; Signal.  
 FT SIGNAL 1 18 POTENTIAL.  
 FT CHAIN 19 343 LUMICAN.  
 FT DOMAIN 40 56 CYS-RICH.  
 FT REPEAT 62 81 LRR-S 1.  
 FT REPEAT 82 105 LRR-T 1.  
 FT REPEAT 106 131 LRR-T 2.  
 FT REPEAT 132 152 LRR-S 2.  
 FT REPEAT 153 176 LRR-T 3.  
 FT REPEAT 177 201 LRR-T 4.  
 FT REPEAT 202 222 LRR-S 3.  
 FT REPEAT 223 246 LRR-T 5.  
 FT REPEAT 247 271 LRR-T 6.  
 FT REPEAT 272 291 LRR-S 4.  
 FT REPEAT 292 321 LRR-T 7.  
 FT REPEAT 322 343 LRR-T 8.  
 FT DISULFID 300 333 BY SIMILARITY.  
 FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (KERATAN SULFATE)

FT CARBOHYD 130 130 (POTENTIAL).  
 FT N-LINKED (GLCNAC. . .) (KERATAN SULFATE)  
 FT (POTENTIAL).  
 FT CARBOHYD 165 165  
 FT N-LINKED (GLCNAC. . .) (KERATAN SULFATE)  
 FT (POTENTIAL).  
 FT CARBOHYD 257 257  
 FT N-LINKED (GLCNAC. . .) (KERATAN SULFATE)  
 FT (POTENTIAL).  
 FT CARBOHYD 320 320  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 343 AA; 38642 MW; A95199C7F32B7C4C CRC64;

Query Match 20.0%; Score 398.5; DB 1; Length 343;  
 Best Local Similarity 31.9%; Pred. No. 1.1e-20;  
 Matches 104; Conservative 72; Mismatches 125; Indels 25; Gaps 9;

QY 67 PFDLFPMCPFG-----CQC---YSRVVHCSDLGLTSVPTNIPDTRMLDLQNNKIK 114  
 Db 24 PADDYGVDFPGSTAPCAPECNCPLSYPTAMYCDNLKLTPI-VPSGIKLYLRRNMIE 82  
 QY 115 EIKENDFKGLTSLGLILNNKL--TKTHKAFILTTKKRLYLSHNLSLSEIPLNLPKSL 172  
 Db 83 SIEENTFDNVTDLQWLILDHNEHLENSKIKGRVFSKLNKLLKHINNLTEAVGPLEPRTL 142  
 QY 173 AELRIHENKVKKIQKDTFKGMNALHVLMSANPLDNGIEGAFEGV-TVFHIRIAEAKL 231  
 Db 143 DDLQLSHNKITKVPNGALEGLVNLTVHLQNNQKADIS-GAFGLNSLLYLDLSFNQL 201  
 QY 232 TSVPRKGLPPTLLELHDYNNKISTVELEDFKRYKELQRLGLGNKKITDIE-NGSLANIPRV 290  
 Db 202 TKLPTGLPHSLMLLYFDNNQISNPDEYFGFKTLQVLRSLSHNKLTDSGIPGVNFTSL 261  
 QY 291 REIHLENNKLLKIPSGLPKLA--YLOIFLHNSIARVGVNDFCTVPKMKKSLYSALS 348  
 Db 262 VELDSLNFQKLSIPTVSENLENFYLQV-----NKINFPJLSSFCVKVGLPYTKITHRL 316  
 QY 349 FNNPVKYMOPATFRVCVLSRMSVOL 374  
 Db 317 DGNLTRLADLPQEMYNCLRVAADISL 342

RESULT 26  
 LUM\_HUMAN STANDARD; PRT; 338 AA.

AC P51884; Q96QW7;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lumican precursor (Keratan sulfate proteoglycan lumican) (KSPG lumican).  
 DE LUM OR LDC.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Cartilage, Intestine, and Placenta;  
 RX MEDLINE=95394964; PubMed=7665616;  
 RA Grover J., Chen X.-N., Korenberg J.R., Roughley P.J.;  
 RT "The human lumican gene. Organization, chromosomal location, and  
 expression in articular cartilage."  
 RL J. Biol. Chem. 270:21942-21949(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Cornea;  
 RX MEDLINE=96047334; PubMed=7558030;  
 RA Chakravarti S., Stallings R.L., Sundarraj N., Cornuet P.K.,  
 Hassell J.R.;  
 RT "Primary structure of human lumican (keratan sulfate proteoglycan)  
 and localization of the gene (LUM) to chromosome 12q21.3-q22.1;"  
 RL Genomics 27:481-488(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Prostate;



RA Strausberg R.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- SUBUNIT: Binds to laminin (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).  
 CC -!- TISSUE SPECIFICITY: Cornea and other tissues.  
 CC -!- DEVELOPMENTAL STAGE: Present in the extracellular matrix of human articular cartilage at all ages, although its abundance is far greater in the adult. In the adult cartilage lumican exists predominantly in a glycoprotein form lacking keratan sulfate, whereas the juvenile form of the molecule is a proteoglycan.  
 CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SLRPS) FAMILY. CLASS II SUBFAMILY.  
 CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).  
 CC -----  
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 CC -----  
 DR EMBL; U18728; AAA85268.1; -;  
 DR EMBL; U21128; AAA91639.1; -;  
 DR EMBL; BC007038; AAH07038.1; -;  
 DR Genew; HGNC:6724; LUM.  
 DR MIM; 600616; -;  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR000372; LRR\_Nterm.  
 DR InterPro; IPR003592; LRR\_Out.  
 DR InterPro; IPR003591; LRR\_Typ.  
 DR Pfam; PF00560; LRR; 9.  
 DR Pfam; PF01462; LRRNT; 1.  
 DR SMART; SM00370; LRR; 4.  
 DR SMART; SM00013; LRRNT; 1.  
 DR SMART; SM00369; LRR\_Typ; 8.  
 DR Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;  
 KW Leucine-rich repeat; Signal.  
 FT SIGNAL 1 18 BY SIMILARITY.  
 FT CHAIN 19 338 LUMICAN.  
 FT DOMAIN 37 53 CYS-RICH.  
 FT REPEAT 59 78 LRR-S 1.  
 FT REPEAT 79 102 LRR-T 1.  
 FT REPEAT 103 128 LRR-T 2.  
 FT REPEAT 129 149 LRR-S 2.  
 FT REPEAT 150 171 LRR-T 3.  
 FT REPEAT 172 196 LRR-T 4.  
 FT REPEAT 197 217 LRR-S 3.  
 FT REPEAT 218 241 LRR-T 5.  
 FT REPEAT 242 266 LRR-T 6.  
 FT REPEAT 267 286 LRR-S 4.  
 FT REPEAT 287 316 LRR-T 7.  
 FT REPEAT 317 338 LRR-T 8.  
 FT DISULFID 295 328 BY SIMILARITY.  
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (KERATAN SULFATE) (POTENTIAL).  
 FT 127 127 N-LINKED (GLCNAC. . .) (KERATAN SULFATE) (POTENTIAL).  
 FT 160 160 N-LINKED (GLCNAC. . .) (KERATAN SULFATE) (POTENTIAL).  
 FT 252 252 N-LINKED (GLCNAC. . .) (KERATAN SULFATE) (POTENTIAL).  
 FT 27 27 L -> P (IN REF. 1).  
 FT CONFLICT 101 101 L -> V (IN REF. 1).  
 SQ SEQUENCE 338 AA; 38429 MW; 905D2ERD370CC59D CRC64;  
 Query Match 19.6%; Score 390; DB 1; Length 338;  
 Best Local Similarity 31.8%; Pred. No. 4.2e-20;  
 Matches 100; Conservative 70; Mismatches 122; Indels 22; Gaps 10;  
 QY 66 PFDFL-----PMPGQC-----YSRVHCSDLGLTSTPTNIPFTRMLDIONNWKIKE 118  
 DB 25 PFLSIYGSSNCAPECNCPESPSAMYCDLKLKSPM-VPPGIKYLYLRNNQIDHIDE 83

QY 119 NDFKGLTSLYLNNKL--TKIHPKAFLT--TKLRRLYLHSHNOLSEIPLNPKSLAE 176  
 DB 84 KAFENVTDLQWLIDHNNLENSKIGRVFSKQLKQLKHLHNNHNLTSVCGPLPKSLEDLQ 143  
 QY 177 IHENKVKIKQDTFKGMNALHVLMSANPLDNNNGIEFGAFEGV-TVFHIRIAEAKLTSP 235  
 DB 144 LTHNKITKL--GSFEGVLNLTFIHLQHNLKEDAVS-AAFKGLKSLLEYLDLSFNQIARLP 200  
 QY 236 KGLPPTLLEHLNDYKISTVEEDFKRYKELQRLGIGLNKKITDIE-NGSLANIPRVREIH 294  
 DB 201 SGLPVSLLTYLDNNKISNPDEYFKRFNALQVLRSLHNLADSGIPGNSFNYSLSVELD 260  
 QY 295 LENNKLKIPSGLPK--YLOIIFLHNSIARVGVNDVCTVTPVKMKKSLYSALSIFNNP 352  
 DB 261 LSYNKLKANIPTVNELENYILEV-----NOLEKFDIKSFCKILOPLYSYKIKHLRDG 315  
 QY 353 VKYEMQPATFRVCV 366  
 DB 316 ISETSLPPDMYECL 329  
 RESULT 27  
 LUM\_BOVIN  
 ID LUM\_BOVIN STANDARD; PRT; 342 AA.  
 AC Q05443;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Luminan precursor (Keratan sulfate proteoglycan) (KSPG) (Corneal  
 DE keratan sulfate proteoglycan 37B core protein).  
 GN LUM OR LDC.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 272-295.  
 RC TISSUE=Cornea;  
 RX MEDLINE=93280153; PubMed=8099356;  
 RA Funderburgh J.L., Funderburgh M.L., Brown S.J., Vergnes J.-P.,  
 RA Hassell J.R., Mann M.M., Conrad G.W.;  
 RT "Sequence and structural implications of a bovine corneal keratan  
 RT sulfate proteoglycan core protein. Protein 37B represents bovine  
 RT lumican and proteins 37A and 25 are unique.";  
 RL J. Biol. Chem. 268:11874-11880(1993).  
 RN [2]  
 RP SEQUENCE OF 19-42.  
 RX MEDLINE=90243714; PubMed=2139877;  
 RA Funderburgh J.L., Conrad G.W.;  
 RT "Isoforms of corneal keratan sulfate proteoglycan.";  
 RL J. Biol. Chem. 265:8297-8303(1990).  
 CC -!- SUBUNIT: Binds to laminin.  
 CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).  
 CC -!- TISSUE SPECIFICITY: Cornea and other tissues.  
 CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SLRPS) FAMILY. CLASS II SUBFAMILY.  
 CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).  
 CC -----  
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 CC -----  
 DR EMBL; L11063; AAA30608.1; -;  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR000372; LRR\_Nterm.  
 DR InterPro; IPR003592; LRR\_Out.  
 DR InterPro; IPR003591; LRR\_Typ.

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DR Pfam; PF00560; LRR; 9.
DR Pfam; PF01482; LRRNT; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00370; LRR; 1.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_TVP; 1.
DR SMART; SM00369; LRR_TVP; 1.
KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal.
FT SIGNAL 1 18
FT CHAIN 19 342
FT DOMAIN 41 57
FT REPEAT 63 82
FT REPEAT 83 106
FT REPEAT 107 132
FT REPEAT 133 153
FT REPEAT 154 175
FT REPEAT 176 200
FT REPEAT 201 221
FT REPEAT 222 245
FT REPEAT 246 270
FT REPEAT 271 290
FT REPEAT 291 320
FT REPEAT 321 342
FT DISULFID 299 332
FT CARBOHYD 92 92
FT CARBOHYD 131 131
FT CARBOHYD 164 164
FT CARBOHYD 256 256
FT CARBOHYD 342 AA; 38756 MW; 592DEE9A49AEB79 CRG64;
SQ SEQUENCE 342 AA; 38756 MW; 592DEE9A49AEB79 CRG64;

Query Match 19.3%; Score 384; DB 1; Length 342;
Best Local Similarity 32.2%; Pred. No. 1.1e-19;
Matches 101; Conservative 68; Mismatches 123; Indels 22; Gaps 10;

QY 66 FPFDFL---PMCPFGQC---YSRVHCSDGLGTSVPTNPDPTRMLDNLNKKIKEIK 118
Db 29 FPQALYGRSSNCAPECNCPESYAMCDLKLKSPM-VPPGKIYLYLRNNQIDHDD 87
QY 119 NDFKGLTSLGLIINNKL--TKTHKAFLLTKRLRLYLHSHNLSQEIPLNLPKSLAE 176
Db 88 KAFENVTDLOWLILDHNLLENKSKIGKVPFKLQKLLHINYNNLTESVGPLPKSLVDLQ 147
QY 177 IHENVKKIOKDTFGKGNALHVLMSANPLDNNNGIEPFAFEGV-TVFHIRIAEAKLTSVP 235
Db 148 LTNNKISKL--GSPDGLVNLTFIHLQHNQLKEDAVS-AALKGLKSLLEYLDLSFNQTKLP 204
QY 236 KGLPPTLLELDYKNKISTVELEDFRYKELQRLGLGNKKITDI-ENGSLANIPRVREIH 294
Db 205 SGLVSLTLYLDNNKISNIPDEYFRFSALQYLRHSHNELADSGVPGNSFNYSLSLELD 264
QY 295 LENNKKIKPSGLPELK--YLOIFLHNSIARVGNDFCPTVPKMKKSLYSALSLENFP 352
Db 265 LSNKLSKISITVNNENLYLEV-----NELEKEDVKSFKLGLPLSYKIKHLRLDGNH 319
QY 353 VKYEMQPATRCV 366
Db 320 ITQTSLPDMVECL 333

RESULT 28
LUM_MOUSE
ID LUM_MOUSE STANDARD; PRT; 338 AA.
AC P51885; Q9CXK0; Q99JZ3;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE lumican precursor (keratan sulfate proteoglycan lumican) (KSPG
DE lumican).
GN LUM OR LDC OR LCN.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cornea;
RX MEDLINE=96006258; PubMed=7558724;
RA Funderburgh J.L., Funderburgh M.L., Hevelone N.D., Stech M.E.,
RA Justice M.J., Liu C.-Y., Kao W.W.-Y., Conrad G.W.;
"Sequence, molecular properties, and chromosomal mapping of mouse
lumican.";
RL Invest. Ophthalmol. Vis. Sci. 36:2296-2303(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Cornea;
RX MEDLINE=96006258; PubMed=7558724;
RA Funderburgh J.L., Funderburgh M.L., Hevelone N.D., Stech M.E.,
RA Justice M.J., Liu C.-Y., Kao W.W.-Y., Conrad G.W.;
"Sequence, molecular properties, and chromosomal mapping of mouse
lumican.";
RL Invest. Ophthalmol. Vis. Sci. 36:2296-2303(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic head;
RX STRAIN=C57BL/6J; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori I., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli R., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombacerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wagner K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBUNIT: Binds to laminin (By similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
CC -!- TISSUE SPECIFICITY: Cornea and other tissues.
CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S79461; AAB35361.1; -.
DR EMBL; AF013262; AAB87767.1; -.
DR EMBL; AK014312; BAB29264.1; -.
DR EMBL; BC005550; AAH05550.1; -.
DR MGD; MGI:109347; Lum.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00560; LRR; 9.
DR Pfam; PF01462; LRRNT; 1.

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DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00370; LRR; 1.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_TYP; 1.
KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
FT SIGNAL 1 18
FT CHAIN 19 338
FT DOMAIN 37 53
FT REPEAT 59 78
FT REPEAT 79 102
FT REPEAT 103 128
FT REPEAT 129 149
FT REPEAT 150 171
FT REPEAT 172 196
FT REPEAT 197 217
FT REPEAT 218 241
FT REPEAT 242 266
FT REPEAT 267 286
FT REPEAT 287 316
FT REPEAT 317 338
FT DISULFID 295 328
FT CARBOHYD 88 88
FT CARBOHYD 127 127
FT CARBOHYD 160 160
FT CARBOHYD 252 252
FT CONFLICT 57 57
FT CONFLICT 109 109
FT CONFLICT 293 293
FT CONFLICT 338 AA; 38265 MW; PF1E050C8979140 CRC64;
SQ SEQUENCE 338 AA; 38265 MW; 13442BAECC905585 CRC64;

Query Match 19.2%; Score 383; DB 1; Length 338;
Best Local Similarity 32.9%; Pred. No. 1.3e-19;
Matches 100; Conservative 66; Mismatches 120; Indels 18; Gaps 9;

QY 72 PNCPCGOC---YSRVHCSDLGTSVPTNIPFDTMLDLONNKIKEIKENDFKGLTSLY 128
Db 35 PNCPCGOC---YSRVHCSDLGTSVPTNIPFDTMLDLONNKIKEIKENDFKGLTSLY 128
QY 129 GLILNNKL--TKIHPKAFLLTKRLRLYLSHNOLSEIPLNPKSLAEIRHENKVKIQ 186
Db 94 WLILDHNLLENSKINGKVFSLKQLKHLHYNLNTESVGLPLKSLQDLQTLNKKISKL- 152
QY 187 KDTFGKMAHLVLENSANPLDNNNGIEGAFGV-TVPHIRIAEAKLTSPVKGLPPTLLEL 245
Db 153 -GSFDGLVNLTFIYLOHNLQKEDAVS-ASLGLKSLEYLDLSFNQMSKLPAGLPTSLTL 210
QY 246 HLDYNNKISTVEDEPKRYKELQRLGLGNKKTIDI-ENGSLANIPRVREIHLNKKKIP 304
Db 211 YLDNKKISNIPDEYKFTGLQYLRSLHNEADSGVGNFNSISLLELDLSYNKKLSIP 270
QY 305 SGLPELK--YIQIIFLHNSIARVGVNDFCTVPKMKKLSYSAISLNNPVKYMOPAT 362
Db 271 TVNENLNNYILEV-----NELEKFDVKSFKILGLSLYSKIKHLRLDGNPLTQSSLPDM 325
QY 363 FCV 366
Db 326 YECL 329

RESULT 29
LUM_RAT
ID LUM_RAT STANDARD; PRT; 338 AA.
AC P51886;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lumican precursor (Keratan sulfate proteoglycan lumican) (KSPG lumican).
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GN LUM OR LDC OR LCN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Eye;
RA Krull N.B.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
CC -|- SUBUNIT: Binds to laminin (By similarity).
CC -|- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
CC -|- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
CC (SLRPS) FAMILY. CLASS II SUBFAMILY.
CC -|- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
CC
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CC
CC EMBL; X84039; CAA58858.1; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00560; LRR; 9.
DR PRINTS; PR001462; LRRNT; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00370; LRR; 1.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_TYP; 1.
KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal.
FT SIGNAL 1 18
FT CHAIN 19 338
FT DOMAIN 37 53
FT REPEAT 59 78
FT REPEAT 79 102
FT REPEAT 103 128
FT REPEAT 129 149
FT REPEAT 150 171
FT REPEAT 172 196
FT REPEAT 197 217
FT REPEAT 218 241
FT REPEAT 242 266
FT REPEAT 267 286
FT REPEAT 287 316
FT REPEAT 317 338
FT DISULFID 295 328
FT CARBOHYD 88 88
FT CARBOHYD 127 127
FT CARBOHYD 160 160
FT CARBOHYD 252 252
FT CARBOHYD 338 AA; 38279 MW; 13442BAECC905585 CRC64;
SQ SEQUENCE 338 AA; 38279 MW; 13442BAECC905585 CRC64;

Query Match 19.0%; Score 378; DB 1; Length 338;
Best Local Similarity 32.2%; Pred. No. 2.9e-19;
Matches 99; Conservative 67; Mismatches 123; Indels 18; Gaps 9;

QY 69 DLFPMPFCGOC---YSRVHCSDLGTSVPTNIPFDTMLDLONNKIKEIKENDFKGLT 125
Db 32 ELSPNCAPECNPHSYPTAMICDDLKLSVPM-VPGIKYLYLRNNOIDHIDEKAFENV 90
QY 126 SLYGLILNNKL--TKIHPKAFLLTKRLRLYLSHNOLSEIPLNPKSLAEIRHENKVK 183
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Db 91 DLQWILDHNLLENSKIGKVFESKQLKHLHINNNLTESVGLPKSLQDLQLANNKIS 150  
 QY 184 KTOKDTFGKGNALHVLMSANPLDNNGIEPCAFEGV-TVPHIRIAEAKLTSPKGLPPTL 242  
 Db 151 KL--GSPDGLVNLFIYLOHNLQEEAVS-ASLGLKSLEYLDSFNQMSKLPAGLTSL 207  
 QY 243 LELHLDYNNKISTVELEDFKRYKELQRLGLGNKITDI--ENGLSANIPRVREIHLENNK 301  
 Db 208 LTYLDNNKITNPDEYFNRTGLYRLSHNELADGVPCGNSFNISLLELDLSYNK 267  
 QY 302 KIPSLPELK--YLIQIFLHNSSTARVGNDFCTVPKMKKSLYSALSLENPNVYEMQ 359  
 Db 268 SIPTVNNLENYLEEV-----NKLEFDVKSFCILGSLYSYKIKHLRDLGNPLTQSSLP 322  
 QY 360 PATRCV 366  
 Db 323 PDMECL 329  
 RESULT 30  
 OMD\_HUMAN  
 ID OMD\_HUMAN STANDARD; PRT; 421 AA.  
 AC Q99983;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Osteomodulin precursor (Osteoadherin) (OSAD) (Keratan sulfate  
 proteoglycan osteomodulin) (KSPG osteomodulin).  
 GN OMD.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 RL [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Osteoblast;  
 RA Ohno I., Hashimoto J., Takaoka K., Ochi T., Okubo K., Matsubara K.;  
 RT "The cloning of a cDNA for novel genes expressed in human  
 osteoblasts";  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 RP SEQUENCE FROM N.A.  
 RA Ohno I., Matsubara K., Okubo K.;  
 RT "Human osteomodulin gene: intron-exon junctions and chromosomal  
 localization.";  
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: May be implicated in biomineralization processes. Has a  
 function in binding of osteoblasts via the alpha(V)beta(3)-  
 integrin (By similarity).  
 CC -!- SUBUNIT: Binds the alpha(V)beta(3)-integrin (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Extracellular matrix (Potential).  
 CC -!- TISSUE SPECIFICITY: Bone-specific.  
 CC -!- PTM: Binds keratan sulfate chains (By similarity).  
 CC -!- PTM: Sulfated on tyrosine residue(s) (By similarity).  
 CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS  
 (SLEURS) FAMILY. CLASS II SUBFAMILY.  
 CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).  
 CC  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: AB000114; BAA19055.1; -  
 CC EMBL: AB009589; BAA23982.1; -  
 CC Genew: HGNC:8134; OMD.  
 CC InterPro: IPR001611; LRR.  
 CC InterPro: IPR000372; LRR\_Nterm.  
 CC InterPro: IPR003592; LRR\_Out.  
 CC InterPro: IPR003591; LRR\_typ.

DR pfam; PF00560; LRR; 7.  
 DR pfam; PF01462; LRRNT; 1.  
 DR SMART; SM00370; LRR; 1.  
 DR SMART; SM00013; LRRNT; 1.  
 DR SMART; SM00369; LRR\_TYP; 1.  
 KW Cell adhesion; Glycoprotein; Extracellular matrix; Proteoglycan;  
 KW Repeat; Leucine-rich repeat; Signal; Sulfation.  
 FT SIGNAL 1 20  
 FT CHAIN 21 421  
 FT DOMAIN 62 78  
 FT REPEAT 84 103  
 FT REPEAT 104 127  
 FT REPEAT 128 153  
 FT REPEAT 154 174  
 FT REPEAT 175 198  
 FT REPEAT 199 224  
 FT REPEAT 225 245  
 FT REPEAT 246 269  
 FT REPEAT 270 292  
 FT REPEAT 293 312  
 FT REPEAT 313 342  
 FT REPEAT 343 367  
 FT DOMAIN 385 409  
 FT DISULFID 321 353  
 FT MOD\_RES 25 25  
 FT MOD\_RES 31 31  
 FT MOD\_RES 39 39  
 FT CARBOHYD 113 113  
 FT CARBOHYD 121 121  
 FT CARBOHYD 187 187  
 FT CARBOHYD 242 242  
 FT CARBOHYD 316 316  
 SQ SEQUENCE 421 AA; 49492 MW; CED47B2BC33BB872 CRC64;  
 Query Match 18.4%; Score 366; DB 1; Length 421;  
 Best Local Similarity 29.3%; Pred. No. 2.5e-18;  
 Matches 95; Conservative 73; Mismatches 138; Indels 18; Gaps 8;  
 QY 41 DDDDDDDDDDDNSLFPTRPRSHFPFDPFPM-CPFGQCQ---YSRVHVCSDGLTSP 96  
 Db 28 DEDYDQDPDDYQTGFPPQNVYGVFPFHYTLGCVSECFCTNFPSSWYCDNRKLTIP 87  
 QY 97 TNIPFTRMLDQNNKIKIKEKDFGJTSYGLILNNKLL--TKHKPAFLTTTKKRL 154  
 Db 88 -NTPMHIOQLYLFQNEIEAVTANFTNATHKEINLHNKIKSQIDYGVFAKLPNLLQL 146  
 QY 155 YLSHNSLPIPLNPKSLAEHLHKNVKKIQKDTFGKGNALHVLMSANPLDNNGIEPG 214  
 Db 147 HLEHNNLEFPFPPKSLERLLGYNEISKLTQTNAMQGLVNLTLMLDLCYNYLHSLKDK 206  
 QY 215 APEGV-TVPHIRIAEAKLTSPKGLPPTLLEHLHDYNNKISTVELEDFKRYKELQRLGN 273  
 Db 207 IFAKWEKLMQLNLCNRLSEMPPLPSSLMYLSLENNSSISSEIPEYFDKLPKLTLRMSH 266  
 QY 274 NKITDIENGLANIPRVREIHLENNKLLK---IPSGLELKYLIQIFLHNSIARVYND 330  
 Db 267 NKLODIPY-NIFNLPNIVLSVGHNKLKQAFYIPRNLEHL-----YLONNEIERMNTV 319  
 QY 331 FCTVTPKMKKSLYSATSLFNNPVK 354  
 Db 320 MCPSIDPLHYHHLTVIRVDQNKLK 343  
 RESULT 31  
 FLRL\_HUMAN  
 ID FLRL\_HUMAN STANDARD; PRT; 646 AA.  
 AC Q9NZUL;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Leucine-rich repeat transmembrane protein FLRTL precursor  
 DE (Fibronectin-like domain-containing leucine-rich transmembrane protein  
 1).

GN FLRT1.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND GLYCOSYLATION.  
 RX MEDLINE=20112755; PubMed=10644439;  
 RA Lacy S.E., Bonnemant C.G., Buzney E.A., Kunkel L.M.;  
 RT "Identification of FLRP1, FLRT2, and FLRT3: a novel family of  
 transmembrane leucine-rich repeat proteins.";  
 RL Genomics 62:417-426(1999).  
 CC -!- FUNCTION: May have a function in cell adhesion and/or receptor  
 CC signaling.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).  
 CC -!- TISSUE SPECIFICITY: Expressed in kidney and brain.  
 CC -!- PTM: N-glycosylated.  
 CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.  
 CC -!- SIMILARITY: CONTAINS 10 LEUCINE-RICH REPEATS (LRR).  
 CC -----  
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 CC -----  
 CC EMBL: AF169675; AAF28459.1; ALT\_INIT.  
 CC Genew; HGNC:3760; FLRT1.  
 DR MIM: 604806; -.  
 DR InterPro: IPR003961; FN\_III.  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR000483; LRR\_Cterm.  
 DR InterPro: IPR000372; LRR\_Nterm.  
 DR InterPro: IPR003592; LRR\_Out.  
 DR InterPro: IPR003591; LRR\_Eyp.  
 DR Pfam: PF00041; fn3; 1.  
 DR Pfam: PF00560; LRR; 7.  
 DR Pfam: PF01462; LRRNT; 1.  
 DR Pfam: PF01463; LRRCT; 1.  
 DR PRINTS: PR00019; LEURICHRPT.  
 DR SMART: SM00370; LRR; 1.  
 DR SMART: SM00082; LRRCT; 1.  
 DR SMART: SM00013; LRRNT; 1.  
 DR SMART: SM00369; LRR\_TYP; 1.  
 KW Transmembrane, Leucine-rich repeat; Repeat; Glycoprotein; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 646  
 FT LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN  
 FT FLRT1.  
 FT DOMAIN 21 524  
 FT TRANSMEM 525 545  
 FT DOMAIN 546 646  
 FT POTENTIAL.  
 FT CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 52 77  
 FT LRR 1.  
 FT REPEAT 78 98  
 FT LRR 2.  
 FT REPEAT 99 121  
 FT LRR 3.  
 FT REPEAT 123 147  
 FT LRR 4.  
 FT REPEAT 148 169  
 FT LRR 5.  
 FT REPEAT 170 192  
 FT LRR 6.  
 FT REPEAT 194 218  
 FT LRR 7.  
 FT REPEAT 219 241  
 FT LRR 8.  
 FT REPEAT 242 264  
 FT LRR 9.  
 FT REPEAT 265 288  
 FT LRR 10.  
 FT FIBRONECTIN TYPE-III.  
 FT DOMAIN 407 485  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 221 227  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 646 AA; 71359 MW; FF2BF5DC3A13C92 CRC64;  
 Query Match 18.28; Score 363.5; DB 1; Length 646;  
 Best Local Similarity 32.78; Pred. No. 6.4e-18;  
 Matches 92; Conservative 51; Mismatches 105; Indels 33; Gaps 7;  
 OY 74 CPFGQCYSRVVHCSDLGLTSVPTNIPDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133

Db 26 CPVSCRCDCNGFIYCNDRLGLTSIPADIPDDATTLYLQNNQI-----N 66  
 QY 134 NNKLTIKHPKAFITTKKLRRLYLISHNQLSEIPLNPKSLAEIRIHENKVKYKOKDFPKM 193  
 Db 67 NAGI-----PDCLKTKVNVQVIYLYENDLDEFINLPSRLHQLQNNVTRTIARDSLARI 122  
 QY 194 NALHVLMSANPLDNNNGIEPGAP-EGVTVFHRIAEAKLTSVPKGLPPTLLLEHLHDYDKI 252  
 Db 123 PLEKLUHLDNNSVSTVSEIEDAFADSKQLKLLFLSRNHLSSIPSGLPHTLEELRDLDDRI 182  
 QY 253 STVELEDFKRYKELQRLGLGNKKITD--IENGSLANIPRVREIHLNKKIKIPSGLP 310  
 Db 183 STIPLHAFKGLNLRRLVLDGNLLANQRIADDTFSLQNLTELSELVSRNSLAAPLNLP- 241  
 QY 311 KYLQIIFLHNSIARVGVNDFCTVPKMKKSLYSALSIFNN 351  
 Db 242 AHLQKLYQDNATISHPYN-----TLAKMRE--LERLDLSNN 276  
 RESULT 32  
 PRLP\_BOVIN STANDARD; PRT; 381 AA.  
 ID PRLP\_BOVIN AC Q9GKN8;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Prolargin precursor (proline-arginine-rich end leucine-rich repeat  
 DE protein).  
 DE GN PRELP.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Articular cartilage;  
 RX MEDLINE=20576219; PubMed=11007795;  
 RA Bengtsson E., Aspegberg A., Heinegaard D., Sommarin Y., Spillmann D.;  
 RT "The amino-terminal part of PRELP binds to heparin and heparan  
 RT sulfate.";  
 RL J. Biol. Chem. 275:40695-40702(2000).  
 RN [2]  
 RP FUNCTION  
 RX PubMed=11847210;  
 RA Bengtsson E., Moergelin M., Sasaki T., Timpl R., Heinegaard D.,  
 RA Aspegberg A.;  
 RT "The leucine-rich repeat protein PRELP binds perlecan and collagens  
 RT and may function as a basement membrane anchor.";  
 RL J. Biol. Chem. 277:15061-15068(2002).  
 CC -!- FUNCTION: May anchor basement membranes to the underlying  
 CC connective tissue.  
 CC -!- SUBUNIT: Binds the basement membrane heparan sulfate proteoglycan  
 CC perlecan and triple helical collagens type I and type II.  
 CC -!- SUBCELLULAR LOCATION: Extracellular matrix.  
 CC -!- DOMAIN: The basic amino-terminal Arg/Pro-rich binds heparin and  
 CC heparan sulfate. Binds collagens type I and type II through its  
 CC leucine-rich repeat domain.  
 CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS  
 CC (SLRPS) FAMILY. CLASS II SUBFAMILY.  
 CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).  
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 CC -----  
 CC EMBL: AF163568; AAG23723.1; -.  
 DR InterPro: IPR001611; LRR.

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DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR003592; LRR_Out.
DR InterPro: IPR003591; LRR_Typ.
DR Pfam: PF00560; LRR: 10.
DR Pfam: PF01462; LRRNT: 1.
DR PRINTS: PR00019; LEURICHRPT.
DR SMART: SM00370; LRR: 7.
DR SMART: SM00013; LRRNT: 1.
DR SMART: SM00369; LRR_Typ: 7.
KW Glycoprotein; Extracellular matrix; Repeat; Leucine-rich repeat;
KW Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 381 PROLARGIN.
FT DOMAIN 72 88 CYS-RICH.
FT REPEAT 94 113 LRR-S 1.
FT REPEAT 114 137 LRR-T 1.
FT REPEAT 138 161 LRR-T 2.
FT REPEAT 162 182 LRR-S 2.
FT REPEAT 183 206 LRR-T 3.
FT REPEAT 207 232 LRR-T 4.
FT REPEAT 233 253 LRR-S 3.
FT REPEAT 254 277 LRR-T 5.
FT REPEAT 278 302 LRR-T 6.
FT REPEAT 303 322 LRR-S 4.
FT REPEAT 323 361 LRR-T 7.
FT REPEAT 362 381 LRR-T 8.
FT DOMAIN 196 201 POLY-LEU.
FT DISULFID 331 372 BY SIMILARITY.
FT CARBOHYD 123 123 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 319 319 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 326 326 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 381 AA; 43682 MW; 23DA99C01BB772A0 CRC64;

Query Match 18.1%; Score 361.5; DB 1; Length 381;
Best Local Similarity 29.7%; Pred. No. 4.6e-18;
Matches 87; Conservative 59; Mismatches 132; Indels 15; Gaps 7;

QY 47 DDDDENSLPTREPRSHFFDLFWPCPGQC---YSRVHCSDLGTSVPTNPFT 103
Db | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
49 DEPTPTDLPPLPPG---PPSVPDCPRECYCPDPFSPALYCDNRNLRKVPV-IPSR 103
QY 104 RMLDLQNKIKETKENDFKGLTSLYGLLNKNTLKHPKAFLTTKKRLRLYLHNQLE 163
Db | | | | | | : | : | : | : | : | : | : | : | : | : | : | : |
104 HYLQNNFTITLPEVSEFKATGLRWLNLDNRIRVDQVLEKLSFLVLEKQLEEE 163
QY 164 IPLNPKSLAELRIHENKVKIKQDTFKGMNALHVLEMSANPLDNGIPEGAFEGV-TYP 222
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
164 VPAALPRNLQRLSQNISRIPIPGVFSKLENLLLDLQHNKLSGCVFKPDTFQGLKML 223
QY 223 HIRIAEAKLTSVPGKLPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNKITD--TE 280
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
224 QLNLAHTLRKMPKVPESAHLQYLDNSRTEAIPSGYFKGFPNLAFIRLNYNQLSDRGLP 283
QY 281 NGLSNIAPRYRETHLENNKLLKIPSGLPKLYLQIIFLHNSIARVGVNDFCP 333
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
284 KNSF-NISNLLVHLNLSNRISVPASSRLEHL---YLNNSIEKINGTQICP 332

RESULT 33
PRLP_HUMAN
ID PRLP_HUMAN STANDARD; PRT; 382 AA.
AC P51888;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Prolargin precursor (Proline-arginine-rich end leucine-rich repeat protein).
DE PRELP.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;

[1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=96029653; PubMed=7592739;
RA Bengtsson E., Neame P.J., Heinegaard D., Sommerin Y.;
RT "The primary structure of a basic leucine-rich repeat protein, PRELP,
RL found in connective tissues.";
RJ J. Biol. Chem. 270:25639-25644 (1995).
[2] SEQUENCE FROM N.A.
RX MEDLINE=97127584; PubMed=8954791;
RA Grover J., Chen X.-N., Korenberg J.R., Recklies A.D., Roughley P.J.;
RT "The gene organization, chromosome location, and expression of a
RL 55-kDa matrix protein (PRELP) of human articular cartilage.";
CC Genomics 38:109-117(1996).
-!- FUNCTION: May anchor basement membranes to the underlying
CC connective tissue (By similarity).
-!- SUBUNIT: Binds the basement membrane heparan sulfate proteoglycan
CC perlecan and triple helical collagens type I and type II (By
CC similarity).
-!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
-!- TISSUE SPECIFICITY: Connective tissue.
-!- DOMAIN: The basic amino-terminal Arg/Pro-rich binds heparin and
CC heparan sulfate. Binds collagens type I and type II through its
CC leucine-rich repeat domain (By similarity).
-!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
CC (SLRPS) FAMILY. CLASS II SUBFAMILY.
-!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
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EMBL; U29089; AAC50230.1; -
EMBL; U41344; AAC18782.1; -
EMBL; U41343; AAC18782.1; JOINED.
Genew; HGNC:9357; PRELP.
MIM; 601914; -
InterPro: IPR001611; LRR.
InterPro: IPR000372; LRR_Nterm.
InterPro: IPR003591; LRR_Typ.
Pfam; PF00560; LRR; 8.
Pfam; PF01462; LRRNT; 1.
SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR_Typ; 1.
KW Glycoprotein; Extracellular matrix; Repeat; Leucine-rich repeat;
KW Signal; Polymorphism.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 382 PROLARGIN.
FT DOMAIN 73 89 CYS-RICH.
FT REPEAT 95 114 LRR-S 1.
FT REPEAT 115 138 LRR-T 1.
FT REPEAT 139 162 LRR-T 2.
FT REPEAT 163 183 LRR-S 2.
FT REPEAT 184 207 LRR-T 3.
FT REPEAT 208 233 LRR-T 4.
FT REPEAT 234 254 LRR-S 3.
FT REPEAT 255 278 LRR-T 5.
FT REPEAT 279 303 LRR-T 6.
FT REPEAT 304 323 LRR-S 4.
FT REPEAT 324 362 LRR-T 7.
FT REPEAT 363 382 LRR-T 8.
FT DOMAIN 197 202 POLY-LEU.
FT DISULFID 332 373 BY SIMILARITY.
FT CARBOHYD 124 124 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 327 327 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 348 348 N -> H (IN DBSNP:9439).
/FTId=VAR_011976.

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DR	InterPro: IPR003592; LRR_out.
DR	InterPro: IPR003591; LRR_typ.
DR	Pfam: PF00560; LRR; 8.
DR	Pfam: PF01462; LRRNT; 1.
DR	PRINTS: PR00019; LEURICHRPT.
DR	SMART: SM00370; LRR; 5.
DR	SMART: SM00013; LRRNT; 1.
DR	SMART: SM00369; LRR_TYP; 8.
KW	Glycoprotein; Extracellular matrix; Repeat; Leucine-rich repeat;
KW	Signal.
FT	SIGNAL. 1 21
FT	CHAIN 22 377
FT	DOMAIN 68 84
FT	REPEAT 90 109
FT	REPEAT 110 133
FT	REPEAT 134 157
FT	REPEAT 158 178
FT	REPEAT 179 202
FT	REPEAT 203 228
FT	REPEAT 229 249
FT	REPEAT 250 273
FT	REPEAT 274 298
FT	REPEAT 299 318
FT	REPEAT 319 357
FT	REPEAT 358 377
FT	DOMAIN 192 197
FT	DISULFID 327 368
FT	CARBOHYD 119 119
FT	CARBOHYD 284 284
FT	CARBOHYD 315 315
FT	CARBOHYD 322 322
FT	CARBOHYD 377 AA; 43179 MW; 79CBE62534753C46 CRC64;
SEQ	SEQUENCE 377 AA; 43179 MW; 79CBE62534753C46 CRC64;
Query Match 17.9%; Score 356.5; DB 1; Length 377;	
Best local similarity 30.7%; Pred. No. le-17;	
Matches 84; Conservative 58; Mismatches 121; Indels 11; Gaps	
QY	67 PFDLFPMPGECQ---YSRVHCHSDGLGTSVPTNPFDTRMLDLONNKIKEIKENDEKG 123
Db	61 PPSVFPDPCREYCPDPFSPALYCDSNLRKVP I-PPRIHYLYLQNNFITELPVESFN 119
QY	124 LTSLYGLILANNKLTIKHPKAFITTKRLRLYLSHNSOLSEIPLNLPKSLAEIRHENKVK 183
Db	120 ATGLRWLNDNNRIRKVDQVRLEKLPGLAFLYMDKNGLEEVSPALPNLEQLSQLNIS 179
QY	184 KIQKDTFGKNALHVLMSANPLDNGIEPGAFEGV-TVPHIRIAEAKLTSVPKGLPPTL 242
Db	180 RIPPVFSKLENLLLDLQHNRLSDGVFKADTFQGLKNLMQLNAHLNLRMPMPKVPPI 239
QY	243 LELHLDYKNTSTVELEDFKRYKELQRLGLGNKKTID--IENGSIANTPRVRETHLENNKL 300
Db	240 HOLYDSNKIETIPSGYFKDFPNLAFIRMYNKLSDRGLPKNSF-NISNLLVHLHSHNK 298
QY	301 KKIPSGPELKYLQIIFLHNSIARVGVDNFCPT 334
Db	299 SNVPAISNKEHL--YLNNSIEKINGTQICPS 329
RESULT 35	
KERA_MOUSE	
ID	KERA_MOUSE STANDARD; PRT; 351 AA.
AC	O35367;
DT	15-JUN-2002 (Rel. 41, Created)
DT	15-JUN-2002 (Rel. 41, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Keratan precursor (KTN) (Keratan sulfate proteoglycan keratan).
GN	KERA OR KTCN.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;	
RP	[1]
RN	SEQUENCE FROM N.A.





(SLRPS) FAMILY, CLASS II SUBFAMILY.  
-!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).  
-----  
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-----  
DR EMBL; X16485; CAA34503.1; .  
DR PIR; S05390; S05390.  
DR InterPro; IPR001611; LRR.  
DR InterPro; IPR000372; LRR\_Nterm.  
DR InterPro; IPR003592; LRR\_out.  
DR InterPro; IPR003591; LRR\_tyr.  
DR Pfam; PF00560; LRR; 8.  
DR Pfam; PF01462; LRRNT; 1.  
DR SMART; SM00370; LRR; 1.  
DR SMART; SM00013; LRRNT; 1.  
DR SMART; SM00013; LRRNT; 1.  
DR SMART; SM00369; LRR\_TYR; 2.  
KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;  
KW Leucine-rich repeat; Signal.  
FT SIGNAL 1 18  
FT CHAIN 19 375  
FT DOMAIN 75 91  
FT REPEAT 97 116  
FT REPEAT 117 140  
FT REPEAT 141 166  
FT REPEAT 167 187  
FT REPEAT 188 211  
FT REPEAT 212 234  
FT REPEAT 235 255  
FT REPEAT 256 279  
FT REPEAT 280 304  
FT REPEAT 305 324  
FT REPEAT 325 354  
FT REPEAT 355 375  
FT DISULFID 333 366  
FT CARBOHYD 126 126  
FT CARBOHYD 165 165  
FT CARBOHYD 200 200  
FT CARBOHYD 290 290  
FT CARBOHYD 340 340  
SQ SEQUENCE 375 AA; 42933 MW; CL2317E825B22B9 CRC64;  
  
Query Match 17.2%; Score 342.5; DB 1; Length 375;  
Best Local Similarity 17.2%; Pred. No. 9.2e-17;  
Matches 103; Conservative 66; Mismatches 158; Indels 45; Gaps 13;  
  
QY 6 LLLFLALCSAK--PFFSPSHALKNMLKMDTDDDDDD-----DDDDDDDDNSLFL- 56  
DB 6 ILLLAGLCSLWAAQYEDSHWFO--FLRNOOSTYDDPDYPPYEPYPTGEGPAYA 63  
QY 57 ----PTREPRSHFPEDFLPMCPGCGCQ---YSRVHCSDLGLTSVPTNPEDFRMLDLQ 109  
DB 64 VGSPQPPRPD-----CPQECDCPPNPFTAMCDNNKLYLFP-VPSRMKYVYFQ 112  
QY 110 NKKTEIKENDFKGITSYGLILNNKLT--KIHPKAFLLTKLRLRYLSHNSQLSEIPLN 167  
DB 113 NNOISSIQGVFNATGLLWIALHGNQITSDKVGKVFESKRLHLRLYLHNNLTRLTPSP 172  
QY 168 LPKSLAEIRIENKVKTKQKDTFGKGNALHVLNANSPLDNGNLEPGAFGV-TVFHRI 226  
DB 173 LPRSURELHNDHNSRYPNNALEGNLTALYLHNEIOEVG---SSMKGLRLSLDL 229  
QY 227 AEAKLTSVPKGLPPTLLEHLHDYKNKISVLEDEKRYKELQRLGINKKLTIDENGSLA- 285  
DB 230 SYNHLRKVPDGLPSALEOYLXLEHNNVSPDSYFGSKPLLYVRLSHNSLT---NGLAS 286  
QY 286 ---NIPRVREHLNENKLIKIPSGLPELKYLIQIIFLHNSNSTARVGVNDFCPTVPMKKSL 342

DB 287 NTENSSSLLLELDLSYNOLQKIP---PVSTNLENLYLQGNRINEFSISFCTVVDVNMFSK 343  
QY 343 YSAISLFNNPVK 354  
DB 344 LQVQRLDGNEIK 355  
  
RESULT 37  
PRLP\_MOUSE  
ID PRLP\_MOUSE STANDARD; PRT; 378 AA.  
AC Q9JK53;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Prolagin precursor (proline-arginine-rich end leucine-rich repeat  
DE protein).  
GN PRELP.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=11731272;  
RA Grover J., Roughley P.J.;  
RT "Characterization and expression of murine PRELP.";  
RL Matrix Biol. 20:555-564(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC Tissue=Salivary gland;  
RA Strausberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: May anchor basement membranes to the underlying  
CC connective tissue (By similarity).  
CC -!- SUBUNIT: Binds the basement membrane heparan sulfate proteoglycan  
CC perlecan and triple helical collagens type I and type II (By  
CC similarity).  
CC -!- SUBCELLULAR LOCATION: Extracellular matrix.  
CC -!- TISSUE SPECIFICITY: Expressed in cartilage throughout both fetal  
CC development and post-natal life. It is also expressed in the  
CC developing embryo prior to skeletogenesis. In adult, highest  
CC expression in lung, lower levels in cardiac and skeletal muscle.  
CC -!- DOMAIN: The basic amino-terminal Arg/Pro-rich binds heparin and  
CC heparan sulfate. Binds collagens type I and type II through its  
CC leucine-rich repeat domain (By similarity).  
CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN  
CC (SLRPS) FAMILY, CLASS II SUBFAMILY.  
CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; AF261888; AAF72994.2; .  
CC EMBL; AF261887; AAF72994.2; JOINED.  
CC EMBL; BC019775; AAH19775.1; .  
CC MGD; MGI:2151110; Prelp.  
CC InterPro; IPR001611; LRR.  
CC InterPro; IPR000372; LRR\_Nterm.  
CC InterPro; IPR003592; LRR\_out.  
CC Pfam; PF00560; LRR; 8.  
CC Pfam; PF01462; LRRNT; 1.  
CC PRINTS; PR00019; LEURICRPT.  
CC SMART; SM00370; LRR; 6.  
CC SMART; SM00013; LRRNT; 1.  
CC SMART; SM00369; LRR\_TYR; 8.  
KW Glycoprotein; Extracellular matrix; Repeat; Leucine-rich repeat;  
KW Signal.





[illegible]











FT REPEAT 206 226 LRR-S 3.  
 FT REPEAT 227 250 LRR-T 5.  
 FT REPEAT 251 275 LRR-T 6.  
 FT REPEAT 276 295 LRR-S 4.  
 FT REPEAT 310 333 LRR-T 7.  
 FT REPEAT 334 353 LRR-T 8.  
 FT CARBOHYD 304 344 BY SIMILARITY.  
 FT CARBOHYD 94 94 N-LINKED (GLCNAC. . .) (KERATAN SULFATE).  
 FT CARBOHYD 168 168 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (KERATAN SULFATE).  
 FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (KERATAN SULFATE).  
 FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 353 AA; CBF42601DF33ED6 CRC64;  
 Query Match 16.3%; Score 325; DB 1; Length 353;  
 Best Local Similarity 31.4%; Pred. No. 1.4e-15;  
 Matches 91; Conservative 50; Mismatches 127; Indels 22; Gaps 10;  
 QY 53 NSLFTPREPSHFFPDLFPMCPFCQCQ---YSRVHCSDLGTSVPTNIPFDTMRMLDQ 109  
 Db 29 NELDP--EHWSH-YTFE---CPQECFCPPSPFNALYCDNKGLEIPA-IPARIWYLYLQ 80  
 QY 110 NNKIKEIKENDFGKTSYGLIILNNKLT--IHPKAFLTTKLRLRYLSHNSLSEIPLN 167  
 Db 81 NNLIETISEKPFVNATHLRWINLNKNKITNNGIESGVLSKLRLLYLFLEDENEEVPAP 140  
 QY 168 LPKSLAEIRIHENKVKTKOKDTFGMNAHLVLEMSANPLDNNGIEPGAFEGV-TVFHRI 226  
 Db 141 LPVGLQELRLARKNISRIPEGVFSNLENITMLDLHQNLLDSALQSDTFQGLNSLMOLNI 200  
 QY 227 AEAKLTSPVKGLPPTLLEHLHDYNKISTVELEDFKRYKELQRLGNNKITD---IENG 283  
 Db 201 AKNSLKKMPLSPANTLQFLDNNISIEVIPENYFSAIPKVTFLRLNKLSDDGIPNG- 259  
 QY 284 LANIPRVREIHLNKKKIPSGLPKYLQIIFLHNSIARVGVNDFCP 333  
 Db 260 -FNVSSILDQLSHNOLTKIP---PINAHLEHLHDHNRKISVNGTQICP 305  
 RESULT 46  
 KERA\_COTJA STANDARD; PRT; 353 AA.  
 AC Q9DE66;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DE Keratocan precursor (KTN) (Keratan sulfate proteoglycan keratocan).  
 GN KERA.  
 OS Coturnix coturnix japonica (Japanese quail).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 OC Coturnix.  
 OX NCBI\_TaxID=93934;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Cornea, and Sclera;  
 RX MEDLINE=20556470; PubMed=11102758;  
 RA Corpeuz L.M., Dunlevy J.R., Hassell J.R., Conrad A.H., Conrad G.W.;  
 RT "Molecular cloning and relative tissue expression of keratocan and  
 RL minican in embryonic quail cornea";  
 RL Matrix Biol. 19:693-698(2000).  
 CC -!- FUNCTION: Play an important role in generating and maintaining a  
 CC transparent matrix within the corneal stroma (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).  
 CC -!- TISSUE SPECIFICITY: Cornea.  
 CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN  
 CC (SLRPS) FAMILY. CLASS II SUBFAMILY.  
 CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AF128223; AAG48156.1; -.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR000372; LRR\_Nterm.  
 DR InterPro; IPR003592; LRR\_out.  
 DR InterPro; IPR003591; LRR\_typ.  
 DR Pfam; PF00560; LRR; 8.  
 DR Pfam; PF01462; LRRNT; 1.  
 DR SMART; SM00370; LRR; 2.  
 DR SMART; SM00013; LRRNT; 1.  
 DR SMART; SM00369; LRR\_TYP; 5.  
 KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;  
 KW Leucine-rich repeat; Signal.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 353 KERATOCAN.  
 FT DOMAIN 43 59 CYS-RICH.  
 FT REPEAT 65 84 LRR-S 1.  
 FT REPEAT 85 108 LRR-T 1.  
 FT REPEAT 109 134 LRR-T 2.  
 FT REPEAT 135 155 LRR-S 2.  
 FT REPEAT 156 179 LRR-T 3.  
 FT REPEAT 180 205 LRR-T 4.  
 FT REPEAT 206 226 LRR-S 3.  
 FT REPEAT 227 250 LRR-T 5.  
 FT REPEAT 251 275 LRR-T 6.  
 FT REPEAT 276 295 LRR-S 4.  
 FT REPEAT 310 333 LRR-T 7.  
 FT REPEAT 334 353 LRR-T 8.  
 FT DISULFID 304 344 BY SIMILARITY.  
 FT CARBOHYD 94 94 N-LINKED (GLCNAC. . .) (KERATAN SULFATE).  
 FT CARBOHYD 168 168 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (KERATAN SULFATE).  
 FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (KERATAN SULFATE).  
 FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 353 AA; 40279 MW; DEE07614FC598F7D CRC64;  
 Query Match 16.3%; Score 325; DB 1; Length 353;  
 Best Local Similarity 31.4%; Pred. No. 1.4e-15;  
 Matches 91; Conservative 50; Mismatches 127; Indels 22; Gaps 10;  
 QY 53 NSLFTPREPSHFFPDLFPMCPFCQCQ---YSRVHCSDLGTSVPTNIPFDTMRMLDQ 109  
 Db 29 NELDP--EHWSH-YTFE---CPQECFCPPSPFNALYCDNKGLEIPA-IPARIWYLYLQ 80  
 QY 110 NNKIKEIKENDFGKTSYGLIILNNKLT--IHPKAFLTTKLRLRYLSHNSLSEIPLN 167  
 Db 81 NNLIETISEKPFVNATHLRWINLNKNKITNNGIESGVLSKLRLLYLFLEDENEEVPAP 140  
 QY 168 LPKSLAEIRIHENKVKTKOKDTFGMNAHLVLEMSANPLDNNGIEPGAFEGV-TVFHRI 226  
 Db 141 LPVGLQELRLARKNISRIPEGVFSNLENITMLDLHQNLLDSALQSDTFQGLNSLMOLNI 200  
 QY 227 AEAKLTSPVKGLPPTLLEHLHDYNKISTVELEDFKRYKELQRLGNNKITD---IENG 283  
 Db 201 AKNSLKKMPLSPANTLQFLDNNISIEVIPENYFSAIPKVTFLRLNKLSDDGIPNG- 259  
 QY 284 LANIPRVREIHLNKKKIPSGLPKYLQIIFLHNSIARVGVNDFCP 333  
 Db 260 -FNVSSILDQLSHNOLTKIP---PINAHLEHLHDHNRKISVNGTQICP 305  
 RESULT 47  
 FMOD\_HUMAN STANDARD; PRT; 376 AA.  
 ID FMOD\_HUMAN AC Q06828; Q15331;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)











GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 24, 2003, 12:22:00 ; Search time 35 seconds  
(without alignments)  
2231.196 Million cell updates/sec

Title: US-09-944-457-2  
Perfect score: 1992  
Sequence: 1 MKEYVLLFLALCAKPFES.....PATFRCVLSRMSVQLGNFGM 379

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

SPTREMBL-21.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1118.5	56.1	370	13 Q9DE04	Q9de04 oreochromis
2	968	48.6	187	4 Q9NXP3	Q9npx3 homo sapien
3	950	47.7	359	13 Q9DE03	Q9de03 oreochromis
4	917	46.0	410	13 Q9DDZ7	Q9ddz7 petromyzon
5	915	45.9	310	13 Q9DDZ8	Q9ddz8 petromyzon
6	869.5	43.6	347	13 Q9DE00	Q9de00 petromyzon
7	865.5	43.4	388	13 Q9DDZ9	Q9ddz9 petromyzon
8	638.5	32.1	224	13 Q9DE01	Q9de01 brachydanio
9	520	26.1	108	11 Q9CTL6	Q9ctl6 mus musculus
10	397.5	20.0	699	4 Q94769	Q94769 homo sapien
11	363.5	18.2	674	4 Q8WVA2	Q8wva2 homo sapien
12	354	17.8	120	13 Q9DE02	Q9de02 brachydanio
13	340.5	17.1	796	11 Q9WVC1	Q9wvc1 rattus norv
14	336	16.9	1525	4 Q9Y5Q7	Q9y5q7 homo sapien
15	336	16.9	1529	4 Q94813	Q94813 homo sapien
16	335	16.8	1512	13 Q9DE36	Q9de36 brachydanio

17	332.5	16.7	1440	5 Q20204	Q20204 caenorhabdi
18	331.5	16.6	623	4 Q96K39	Q96k39 homo sapien
19	331.5	16.6	649	4 Q96KB1	Q96kb1 homo sapien
20	331.5	16.6	662	4 Q9P259	Q9p259 homo sapien
21	331.5	16.6	1521	11 Q9RLB9	Q9rlb9 mus musculus
22	331	16.6	1530	13 Q90WZ3	Q90wz3 xenopus lae
23	329	16.5	1521	4 Q95710	Q95710 homo sapien
24	329	16.5	1531	11 Q9WVB5	Q9wvb5 mus musculus
25	328	16.5	1534	4 Q75093	Q75093 homo sapien
26	326	16.4	1504	5 Q9V7F9	Q9v7f9 drosophila
27	325	16.3	1523	11 Q9WVB4	Q9wvb4 mus musculus
28	324	16.3	1480	5 Q9V7F8	Q9v7f8 drosophila
29	324	16.3	1523	11 Q88280	Q88280 rattus norv
30	323	16.2	1531	11 Q88279	Q88279 rattus norv
31	320	16.1	798	4 Q8WWZ2	Q8wwz2 homo sapien
32	320	16.1	1504	5 Q9XIV4	Q9xyv4 drosophila
33	319	16.0	1530	11 Q9WUG5	Q9wug5 rattus norv
34	311.5	15.6	1515	13 Q9DE37	Q9de37 brachydanio
35	309	15.5	1523	4 Q75094	Q75094 homo sapien
36	304.5	15.3	581	6 Q9BGP6	Q9bgp6 macaca fasc
37	304.5	15.3	581	6 Q95KI8	Q95ki8 macaca fasc
38	297.5	14.9	581	4 Q8TF66	Q8tf66 homo sapien
39	296	14.9	1091	11 P70193	P70193 mus musculus
40	289	14.5	1093	4 Q96JA1	Q96ja1 homo sapien
41	289	14.5	1094	4 Q9BYB8	Q9byb8 homo sapien
42	287	14.4	96	11 Q63156	Q63156 rattus norv
43	282.5	14.2	391	11 Q9D3K0	Q9d3k0 mus musculus
44	282.5	14.2	1025	11 Q9Z166	Q9z166 mus musculus
45	282	14.2	1095	13 Q90XG4	Q90xg4 gallus gall
46	281.5	14.1	578	11 Q8R5W3	Q8r5m3 rattus norv
47	281	14.1	542	5 Q9N4G6	Q9n4g6 caenorhabdi
48	276.5	13.9	1513	5 Q9VPF0	Q9vpf0 drosophila
49	276	13.9	603	11 Q70211	Q70211 rattus norv
50	275	13.8	522	4 Q96DN1	Q96dn1 homo sapien

#### ALIGNMENTS

RESULT 1

Q9DE04 PRELIMINARY; PRT; 370 AA.  
ID Q9DE04;  
AC Q9DE04;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Biglycan-like protein 3.  
GN BGL3.

OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidel;  
OC Cichlidae; Oreochromis.  
OX NCBI\_TaxID=8128;  
RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=20496956; PubMed=11040287;  
RA Shintani S., Sato A., Toyosawa S., O'Huigin C., Klein J.;  
RT "Biglycan-like extracellular matrix genes of agnathans and teleosts.";  
RL J. Mol. Evol. 51:363-373(2000).  
DR EMBL: AF247821; AAG40156.1; -  
DR InterPro: IPR001611; LRR.  
DR InterPro: IPR000372; LRR\_Nterm.  
DR InterPro: IPR003592; LRR\_Out.  
DR InterPro: IPR003591; LRR\_Lyp.  
DR Pfam: PF00560; LRR: 9.  
DR Pfam: PF01462; LRRNT: 1.  
DR SMART: SM00370; LRR: 2.  
DR SMART: SM00013; LRRNT: 1.  
DR SMART: SM00369; LRR\_TYP: 5.  
SQ SEQUENCE 370 AA; 42177 MW; BCD0675694EAC2B7 CRG64;

Query Match 56.1%; Score 1118.5; DB 13; Length 370;

Best Local Similarity 56.7%; Pred. No. 7e-72;  
Matches 219; Conservative 52; Mismatches 88; Indels 27; Gaps 4;

QY 1 MKEYVLLLLFALCSAKPPSPSHIA--LKN-----MMLKMDTDDDDDDDDDDDDDE 51  
Db 1 MRIFLLCLLALGNKPK-YQINWMDYLNKNTDKIHEIMISDNDDDDDDDDDDDDD 59

QY 52 DNSLFPPTREPSHFFPDLFPMCPFGCCYSRVVHCSDLGLTSVPTNIPDTRMLDLQNN 111  
Db 60 YND-----EDCPAHCHCSPRVVQCSQDGLISVPDKIPEDTVMIDLQNN 102

QY 112 KIKEIKENDFKGLTSYGLIINNKKLKIHPKAFITTKLRRLYLSHNSQSEIPLNPKS 171  
Db 103 DITEFOODDFGLNKLKYLGLFINNKISRIHPKAFKNDNLRLYLSHNSQSEIPLNPPN 162

QY 172 LAELIHNKVKYKOKDFKGMNALHVLMSANPLDNGIPGAFEGTVFHIRIAEAKL 231  
Db 163 VIELRFHENQIDRIKDAFKGLKRLHVLGALNPLTNSGIEGAFGLSTLYIGIAEAKL 222

QY 232 TSVPGKLPPTLHLDYNNKISTVELEDFKRYKELQRLGLGNKKITDIENGLANIPRVR 291  
Db 223 TSIPKDFPSSITSLDYNKISKVEIEDFIRYKNLQRLGLAFNQIKYVENGSLANTPKIR 282

QY 292 EHLNENKLLKIPSGLPKLYLOIFLHNSIARVNDGCTVPKMKKSLYSALSIFNN 351  
Db 283 EYLDNNRMKVPGLSLRLYQVIFLHGNKISSVGINDFCPIRADSKKNPYTGISLFAN 342

QY 352 PVKYWEMQPATRCVLSRMSVOLGNF 377  
Db 343 PVKYWAIQPATRCVTCGRRGVOLGNF 368

RESULT 2  
Q9NXP3  
ID Q9NXP3 PRELIMINARY; PRT; 187 AA.  
AC Q9NXP3;  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE CDNA FLJ20129 fis, clone COL06190.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=COLON;  
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
RA Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,  
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;  
RT "NEDO human cDNA sequencing project."  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK00136; BAA90967.1;  
DR InterPro; IPR001611; LRR.  
DR Pfam; PF00560; LRR; 3.  
SQ SEQUENCE 187 AA; 21074 MW; BDBEE37373CA3DBE CRC64;

Query Match 48.6%; Score 968; DB 4; Length 187;  
Best Local Similarity 100.0%; Pred. No. 1.6e-61;  
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 MNALHVLMSANPLDNGIEPGAEGTVFHIRIAEAKLTSVPKGLPPTLHLDYNNKI 252  
Db 1 MNALHVLMSANPLDNGIEPGAEGTVFHIRIAEAKLTSVPKGLPPTLHLDYNNKI 60

QY 253 STVELEDFKRYKELQRLGLGNKKITDIENGLANIPRVEIHLNENKLLKIPSGLPKLY 312  
Db 61 STVELEDFKRYKELQRLGLGNKKITDIENGLANIPRVEIHLNENKLLKIPSGLPKLY 120

QY 313 LQIIFLHNSIARVNDGCTVPKMKKSLYSALSIFNNPVKYWEMQPATRCVLSRMSV 372  
Db 121 LQIIFLHNSIARVNDGCTVPKMKKSLYSALSIFNNPVKYWEMQPATRCVLSRMSV 180

QY 373 QLGNFGM 379  
Db 181 QLGNFGM 187

RESULT 3  
Q9DE03  
ID Q9DE03 PRELIMINARY; PRT; 359 AA.  
AC Q9DE03;  
DT 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
DE Decorin.  
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;  
OC Cichlidae; Oreochromis.  
OX NCBI\_TaxID=8128;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=20496956; PubMed=11040287;  
RA Shintani S., Sato A., Toyosawa S., O'hugin C., Klein J.;  
RT "Biglycan-like extracellular matrix genes of agnathans and teleosts."  
RL J. Mol. Evol. 51:363-373(2000).  
DR EMBL; AF247822; AAG40157.1; -.  
DR InterPro; IPR001611; LRR.  
DR InterPro; IPR00372; LRR\_Nterm.  
DR InterPro; IPR003592; LRR\_out.  
DR InterPro; IPR003591; LRR\_typ.  
DR Pfam; PF00560; LRR; 7.  
DR Pfam; PF01462; LRRNT; 1.  
DR SMART; SM00370; LRR; 3.  
DR SMART; SM00013; LRRNT; 1.  
DR SMART; SM00369; LRR\_TYP; 7.  
SQ SEQUENCE 359 AA; 39807 MW; F149F9AA4E7572C6 CRC64;

Query Match 47.7%; Score 950; DB 13; Length 359;  
Best Local Similarity 50.8%; Pred. No. 6.7e-60;  
Matches 189; Conservative 57; Mismatches 102; Indels 24; Gaps 4;

QY 7 LLLFALCSAKPPSPSHIALKNMMLKMDTDDDDDDDDDDDDNSLFPTRPSRSHFF 66  
Db 8 LLLVACWALPFRQSGFL--DFMM-----EDGSGDPVTEPLP----- 44

QY 67 PFDLFPMPFGCCYSRVVHCSDLGLTSVPTNIPDTRMLDLQNNKIKEIKENDFKGLTS 126  
Db 45 PVIGGPKCFRCQCHLRVLIQCSDLGLKAVPEDIPDDTLLDLQNNKITEIKENDFKNLG 104

QY 127 LYLIIINNKKLTIHPKAFITTKLRRLYLSHNSQSEIPLNPKSLAEIRIHENKVKIQ 186  
Db 105 LHALILVNNKLTIIHPKAFISPLTKLQRLYLSHNSQSEIPLNPKSLAEIRIHENKVKIK 164

QY 187 KDTFKGMNALHVLMSANPLDNGIEPGAEGV-TVFHIRIAEAKLTSVPKGLPPTLLEL 245  
Db 165 KASFGQMSHVIWELGNSNPLKTAGIAGAFADLKASYIRIADTNITEVPKGLPSLSEL 224

QY 246 HLDYNNKISTVELEDFKRYKELQRLGLGNKKITDIENGLANIPRVEIHLNENKLLKIPS 305  
Db 225 HLDGNNKITLTDRLKGMKNLAKLGLSYNQISSVENGTLSNAPHLRELHLDNALTYSVP 284

QY 306 GPELKYLOIIFLHNSIARVNDGCTVPKMKKSLYSALSIFNNPVKYWEMQPATRC 365  
Db 285 GLPDHKYIOVYLHAKIAAVGTEDFCPPGFTKKAMYSGLISLFPVYWEQVPTFC 344

QY 366 VLRSRMSVOLGNF 377  
Db 345 VFDRSAIQLGNY 356

RESULT 4  
Q9DDZ7  
ID Q9DDZ7 PRELIMINARY; PRT; 410 AA.





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DR Pfam: PF00560; LRR; 8.
DR Pfam: PF01462; LRRNT; 1.
DR SMART: SM00370; LRR; 4.
DR SMART: SM00013; LRRNT; 1.
DR SMART: SM00369; LRR_TYP; 6.
FT NON_TER 1
SQ SEQUENCE 347 AA; 38266 MW; 55CC296938CED391 CRC64;

Query Match 43.6%; Score 869.5; DB 13; Length 347;
Best Local Similarity 54.3%; Pred. No. 3.4e-54;
Matches 165; Conservative 54; Mismatches 84; Indels 1; Gaps 1;

QY 74 CPFGQCYSRVVHCSDLGLTSVPTNIPDTRMLDLQNNKIKEIKENDPKGLTSLYGLILN 133
DB 81 CPFGQCYSRVVHCSDLGLTSVPTNIPDTRMLDLQNNKIKEIKENDPKGLTSLYGLILN 140
QY 134 NKKLTKIHPKAFLTTKLRRLLYLSHNLSEIPLNLPKSLAEALRTHENKVKIKQDTPKGM 193
DB 141 NMLIAKIHPKAFAPVWSLDKLIYSHNRLTEVPTGIPPSLIELRVHENLIKRVPKDTEFINN 200
QY 194 NALHVLMSANPLDNNNGIEPGAFEGV-TVFHIRIAEAKLTSPKGLPPTLLEHLHDYNKI 252
DB 201 GRHLVIELGKNPLPSSGIEVGAENGDLKLTIVIRISYKLTQLPKLPNSLLEHLEGNEI 260
QY 253 STVELEDFKRYKELQRLGLGNKKTIDTENGSLANIPRVREIHLNKKLTKIPSGLPKLY 312
DB 261 VAIEDEDLFGYPYLFRLGLSYNKTITEVQNGSLAVSGNLRDLNNDLVSPGSLKIRS 320
QY 313 LQITFLHSNSTARVGVNDFCPTVPKMKKSLYSALISLFPNNPVKYWEMOPATFCVLSRMSV 372
DB 321 LNVYLHSNKIKEVKTDFCPTVPSPKRAQYAGISLYDNPVKYWEVPPSFCVHNHNAI 380
QY 373 QLGN 376
DB 381 HFGS 384

RESULT 8
Q9DD29 PRELIMINARY; PRT; 388 AA.
AC Q9DD29;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Biglycan-like extracellular matrix genes of agnathans and teleosts."
GN BGL1.
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20496956; PubMed=11040287;
RA Shintani S., Sato A., Toyosawa S., O'hugin C., Klein J.;
RT "Biglycan-like extracellular matrix genes of agnathans and teleosts."
RL J. Mol. Evol. 51:363-373(2000).
DR EMBL: AF247826; AAG40161.1; -.
DR InterPro: IPR001611; LRR.
DR ZFIN: ZDB-GENE-010102-1; Gcn.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR003592; LRR_out.
DR InterPro: IPR003591; LRR_Typ.
DR Pfam: PF00560; LRR; 8.
DR PRINTS: PR00019; LEURICHRPT.
DR SMART: SM00370; LRR; 5.
DR SMART: SM00369; LRR_TYP; 7.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 224 AA; 24442 MW; 54A1B7AB91667DF0 CRC64;

Query Match 32.1%; Score 638.5; DB 13; Length 224;
Best Local Similarity 56.5%; Pred. No. 5.6e-38;
Matches 126; Conservative 37; Mismatches 59; Indels 1; Gaps 1;

QY 94 SVPTNIPDTRMLDLQNNKIKEIKENDPKGLTSLYGLILNKKLTKIHPKAFLTTKLRR 153
DB 2 TVPEKIPDLDTLLDLQNNKITEIKENDPKGLTSLYGLILNKKLTKIHPKAFLTTKLRR 61
QY 154 LYLHNSQLSEIPLNLPKSLAEALRTHENKVKIKQDTPKGMNHALHVLMSANPLDNNNGIEP 213
DB 62 LYLHNSQLSEIPLNLPKSLAEALRTHENKVKIKQDTPKGMNHALHVLMSANPLDNNNGIEP 121
QY 214 GAFEGV-TVFHIRIAEAKLTSPKGLPPTLLEHLHDYNKISTVELEDFKRYKELQRLGLG 272
DB 122 GAFADLKRVSATRIADTNLTSPKGLPPTLLEHLHDYNKISTVELEDFKRYKELQRLGLG 181

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QY 273 NKKITDIENGSLANIPRVREIHLNKKLKKIPSGLPKYLQI 315  
 Db 182 HNEISVWENGSLANVPHRLHLENNALTA VPAGLADHKYIQV 224

## RESULT 9

Q9CTL6 PRELIMINARY; PRT; 108 AA.  
 AC Q9CTL6;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE 4631401G09Rik protein (Fragment).  
 GN ASPN OR 4631401G09RIK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=EYEBALL;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaeerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690(2001).  
 DR EMBL; AK021386; BAB32393.1; -;  
 DR MGD; MGI:1913945; Aspn.  
 DR InterPro; IPR000372; LRR\_Nterm.  
 DR Pfam; PF01462; LRRNT; 1.  
 DR SMART; SM00013; LRRNT; 1.  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 12303 MW; 0BD4358D35949FFA CRC64;

Query Match 26.1%; Score 520; DB 11; Length 108;  
 Best Local Similarity 84.2%; Pred. No. 6.3e-30;  
 Matches 96; Conservative 6; Mismatches 6; Indels 6; Gaps 1;

QY 1 MKEYVLLFLALCSAKPFFPSHTALKNMMLKMDMTDDDDDDDDDDSLFPTR 60  
 Db 1 MKEYVMLLLAVCSAKPFPSPHTALKNMMLKMDMTDDDDDDDDDDSLFPTR 54  
 QY 61 PRSHFFPDLPFCGFCQCYRVVHCSGLTSVPTNIPFDTRMLDLQNNKIK 114  
 Db 55 PVNPFPPDLPFCGFCQCYRVVHCSGLTSVPTNIPFDTRMLDLQNNKIK 108

## RESULT 10

Q94769 PRELIMINARY; PRT; 699 AA.  
 AC Q94769;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Extracellular matrix protein.  
 GN ECM2.

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99009324; PubMed=9790758;  
 RA Nishiu J., Tanaka T., Nakamura Y.;  
 RT "Identification of a novel gene (ECM2) encoding a putative  
 RT extracellular matrix protein expressed predominantly in adipose and  
 RT female-specific tissues and its chromosomal localization to 9q22.3.";  
 RL Genomics 52:378-381(1998).  
 DR EMBL; AB011792; BAA33958.1; -;  
 DR InterPro; IPR001611; LRR;  
 DR InterPro; IPR003592; LRR\_out.  
 DR InterPro; IPR001007; VWF\_C.  
 DR Pfam; PF00560; LRR; 11.  
 DR Pfam; PF00093; vwc; 1.  
 DR PRINTS; SM00019; LEURICHRPT.  
 DR SMART; SM00370; LRR; 4.  
 DR SMART; SM00214; VWC; 1.  
 DR PROSITE; PS01208; VWF; UNKNOWN\_1.  
 KW Matrix protein.

SQ SEQUENCE 699 AA; 79789 MW; E44E76A40A5C2742 CRC64;

Query Match 20.0%; Score 397.5; DB 4; Length 699;  
 Best Local Similarity 24.9%; Pred. No. 3.1e-20;  
 Matches 108; Conservative 77; Mismatches 148; Indels 101; Gaps 8;  
 QY 32 KMDTDDDDDDDDDDDDNSL-----FPTREPSHFFFDLFP-----MCPFGC 78  
 Db 270 EEEDEEEEGEEDEDEEDFVRGDMFMRSP-----LPAPRGTLRLPSCG 320  
 QY 79 QCVSRVHCSGLTSVPTNIPDTRMLDLQNNKIKEIKENDFKGLTSYGLILNNKLT 138  
 Db 321 SLSYRTISCNAMLTQIPPLTAPQITSLELTGNSIASIPDEAFNGLNLERLDLSKNIT 380  
 QY 139 K--IHPKAFLTTKKRLRLVLSHNLSEIPLNLPKSLAEIRIHNKVKIKQDTFGKMNAL 196  
 Db 381 SSGIGPKAFKLLKMLRLNDGNNLIQISQLPSTLEELKYVNNNQADDESLSDLNQL 440  
 QY 197 HVLEMSANPLDNNIGEPAGEV-TVFHIRIAEAKLTSVPKGLPPTLLEHLHDYKISTV 255  
 Db 441 VTLEEGNNLSEANVNPFLAKPLKSLAYRLGKNKFRIPQGLPGSIEELYNNQIERI 500  
 QY 256 ELEDKRYKELQRLGLGNNKI-----TDIENGSLANIP-----288  
 Db 501 TEICFNHTRKINIVILRYNKNIEPNRIAPLAWINQENLESIDLSYNKLHYVPSYLPKSLH 560  
 QY 289 -----RVREIHLNKKL 300  
 Db 561 LVLLGNQIERIPGVVFGHMEPGLEYLYLSFNKLADGMDRVSEFYGAYHSIRLEFLDNDL 620  
 QY 301 KKTIPSGLPKYLQIITFLHSNSTARVGVNDFCTVPKMKKSLYSALSIFNNPVKWMOP 360  
 Db 621 KSIPPGIQEMKALHFLRLNNKIRNLPEEIC-NAEEDDDSNLEHLHLENNYIKIREIFS 679  
 QY 361 ATRCVLSRMSVOL 374  
 Db 680 YTFCSIRSYSSIVL 693

## RESULT 11

Q8WVA2 PRELIMINARY; PRT; 674 AA.  
 AC Q8WVA2;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Hypothetical 74.1 kDa protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

ZFIN; ZDB-GENE-010131-5; bg13.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR003592; LRR\_out.  
 DR InterPro; IPR003591; LRR\_typ.  
 DR Pfam; PF00560; LRR; 4.  
 DR SMART; SM00370; LRR; 3.  
 DR SMART; SM00369; LRR\_TYP; 4.  
 FT NON\_TER 1  
 FT NON\_TER 120 120  
 SQ SEQUENCE 120 AA; 13569 MW; 37A302FB59F97696 CRC64;  
  
 Query Match 17.8%; Score 354; DB 13; Length 120;  
 Best Local Similarity 56.8%; Pred. No. 4.7e-18;  
 Matches 67; Conservative 26; Mismatches 25; Indels 0; Gaps 0;  
  
 QY 95 VPTNPFDTRMLDLQNNKKEIKENDFKGLTSLYGLIINNKKLKIHPKALTTKKLRRL 154  
 DB 2 VPKDIPANTLLDLQNNDIKEKDDFKGLDNLIALFLLNNQISKIHPKAFRMDKKIL 61  
 QY 155 YLSHNOLSEIPLNPKSLAEIRHENKVKIKOTDFKGMNALHVLSEANPLDNGIE 212  
 DB 62 HLSYNLLTOWPENLPIVSQSLRHDHKNKISRLPKGAFKGMHDLNVLELSANPLANS 119  
  
 RESULT 13  
 Q9WVC1 PRELIMINARY; PRT; 796 AA.  
 ID Q9WVC1  
 AC Q9WVC1  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE SLIT-2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE DAWLEY;  
 RX MEDLINE=99292758; PubMed=10364234;  
 RA Liang Y., Annan R.S., Carr S.A., Popp S., Mevissen M., Margolis R.K.,  
 RA Margolis R.U.;  
 RT "Mammalian homologues of the Drosophila slit protein are ligands of  
 the heparan sulfate proteoglycan glypican-1 in brain."  
 RL J. Biol. Chem. 274:17885-17892(1999).  
 DR EMBL; AF141386; RAD38940.2; -.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR000483; LRR\_Cterm.  
 DR InterPro; IPR000372; LRR\_Nterm.  
 DR InterPro; IPR003592; LRR\_out.  
 DR InterPro; IPR003591; LRR\_typ.  
 DR Pfam; PF00560; LRR; 13.  
 DR Pfam; PF01463; LRRCT; 3.  
 DR Pfam; PF01462; LRRNT; 4.  
 DR PRINTS; PR00019; LEURICHRPT.  
 DR SMART; SM00370; LRR; 7.  
 DR SMART; SM00082; LRRCT; 3.  
 DR SMART; SM00013; LRRNT; 4.  
 DR SMART; SM00369; LRR\_TYP; 4.  
 SQ SEQUENCE 796 AA; 89542 MW; 0F50806FC0345005 CRC64;  
  
 Query Match 17.1%; Score 340.5; DB 11; Length 796;  
 Best Local Similarity 26.1%; Pred. No. 4.1e-16;  
 Matches 111; Conservative 55; Mismatches 120; Indels 139; Gaps 13;  
  
 QY 74 CPGCOCYSRVVHCSDGLTSVPTNIPPTDPTLTLNQLI-----RMLDL 108  
 DB 277 CPIATCSNNIVDCRGKLTETPTNLP-ETITEIRLEQNSIRVPPGAFSPYKKLRRLDL 335  
 QY 109 ONNKKIKEIKENDFKGLTSLYGLIINNKKLTKIHPKALTTKKLRRLYLSHNOLSEIPLN 168  
 DB 336 SNNQISELAPDAFGGRLNSLVLYGNKLTETLTPKSLFEGFLSQLLLLNANKINLRVDA 395

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QY 169 PKSLAELR---IHENKVKIKQDFTFGMNAHVLEMSANP-----LDNGIE 212
D 169 PKSLAELR---IHENKVKIKQDFTFGMNAHVLEMSANP-----LDNGIE 212
Db 396 FQDLHNLNLLSYDNKLTQVAKGTFSAIRAIQTMHLAQNPFICDCHLKWLDYLTNPTE 455
QY 213 -PGA-----FEQVTVFH 223
Db 456 TSARCTSPRLANKRIGQIKSKKFCSTEDYRSKLSGDCFADLACPEKRCGGTV-- 513
QY 224 IRIAEAKLTVSPKGLPPTLLEHLHDYKISTVELED-FKRYKELQRLGLGNKNTIDIEG 282
Db 514 -DCSNQKLNKIPHIPOYTAELRNNEFTVLEATGIFKLPQLRKINLNKNTIDIEG 572
QY 283 SLANIPRVREIHLNKKLK-----KIPSGLPKLYLQIIFLHNSIARVGVNDPCPTVPM 338
Db 573 AFEAGSGVNEILLTSNRLENVQHKMFKGLESLKTL---MLRNSRISCVGNDSTGLGSRV 629
QY 339 KKSLEY-----SAISLFPNPVKYWMOPATFRC-----VLSRMS 371
Db 630 LLSLYDNQITTVAPGAFGLHLSLTLNLLANP-----FNCNCHLAWLGEWLRRKR 679
QY 372 VOLGN 376
Db 680 IVTGN 684

RESULT 14
QY507
ID QY507 PRELIMINARY; PRT; 1525 AA.
AC QY507;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE SLIT2.
GN SLIT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=99200389; PubMed=10102266;
RA Wang K.H., Brose K., Arnott D., Kidd T., Goodman C.S., Henzel W.,
RA Tessier-Lavigne M., Kidd T.;
RT "Purification of an axon elongation- and branch-promoting activity
RT from brain identifies a mammalian Slit protein as a positive regulator
RT of sensory axon growth."
RL Cell 96:771-784(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=99200391; PubMed=10102268;
RA Brose K., Bland K.S., Wang K.H., Arnott D., Henzel W., Goodman C.S.,
RA Tessier-Lavigne M., Kidd T.;
RT "Slit proteins bind Robo receptors and have an evolutionarily
RT conserved role in repulsive axon guidance."
RL EMBL; AF133270; RAD25539.1; -.
DR HSSP; P00743; ICCF.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF-2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR003645; FOLN.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00008; EGF; 9.
DR Pfam; PF00054; laminin_G; 1.

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DR Pfam; PF00560; LRR; 17.
DR Pfam; PF01463; LRRCT; 4.
DR Pfam; PF01462; LRRNT; 4.
DR SMART; SM00041; CT; 1.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00001; EGF_like; 7.
DR SMART; SM00274; FOLN; 2.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00370; LRR; 6.
DR SMART; SM00082; LRRCT; 4.
DR SMART; SM00013; LRRNT; 4.
DR SMART; SM00369; LRR_TYP; 8.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_2.
DR PROSITE; PS01185; CTCK_1; UNKNOWN_1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_9.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS01187; EGF_CA; 2.
DR Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
KW SEQUENCE 1525 AA; 169394 MW; 8A81CDE34EF06A73 CRC64;

Query Match 16.9%; Score 336; DB 4; Length 1525;
Best Local Similarity 26.5%; Pred. No. 1.9e-15;
Matches 105; Conservative 61; Mismatches 120; Indels 110; Gaps 12;

QY 74 CPFGCQCYRVVHCGSLGTSVPTNIPDPT-----RMLDL 108
D 74 CPFGCQCYRVVHCGSLGTSVPTNIPDPT-----RMLDL 108
Db 277 CPAACTCSNNIVDCRGKGLTEIPTNLP-ETITEIRLEONTIKVPPGAFSPYKLRIDL 335
QY 109 QNNKIKEKENDFKGLTSLYGLILNKKLTKIHPKAFITTKLRLRLYLSHNLSEIPLNL 168
D 109 QNNKIKEKENDFKGLTSLYGLILNKKLTKIHPKAFITTKLRLRLYLSHNLSEIPLNL 168
Db 336 SNNQISELAPDAFQGLRSLNLSLVYGNKITELPKSLPGLFSLQLLLNANKINCLRDA 395
QY 169 PKSLAELR---IHENKVKIKQDFTFGMNAHVLEMSANP-----LDNGIE 212
D 169 PKSLAELR---IHENKVKIKQDFTFGMNAHVLEMSANP-----LDNGIE 212
Db 396 FQDLHNLNLLSYDNKLTQIAGTFSPLRAIQTMHLAQNPFICDCHLKWLDYLTNPTE 455
QY 213 -PGA-----FEQVTVFH 223
Db 456 TSARCTSPRLANKRIGQIKSKKFCSTEDYRSKLSGDCFADLACPEKRCGGTV-- 513
QY 224 IRIAEAKLTVSPKGLPPTLLEHLHDYKISTVELED-FKRYKELQRLGLGNKNTIDIEG 282
Db 514 -DCSNQKLNKIPHIPOYTAELRNNEFTVLEATGIFKLPQLRKINLNKNTIDIEG 572
QY 283 SLANIPRVREIHLNKKLK-----KIPSGLPKLYLQIIFLHNSIARVGVNDPCPTVPM 338
Db 573 AFEAGSGVNEILLTSNRLENVQHKMFKGLESLKTL---MLRNSRITCVGNDSF-----I 623
QY 339 KKSLEY-----SAISLFPNPVKYWMOPATFRCVLSRMSVOL 374
Db 624 GLSSVRLSLYDNQIT--TVAPGAFDTLHLSLTLN 657

RESULT 15
QY4813
ID QY4813 PRELIMINARY; PRT; 1529 AA.
AC QY4813;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Slit-2 protein.
GN Slit-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99033071; PubMed=9813312;
RA Itoh A., Miyabayashi T., Ohno M., Sakano S.;
RT "Cloning and expressions of three mammalian homologues of drosophila
RT slit suggest possible roles for slit in the formation and maintenance

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RT of the nervous system."  
RL Brain Res. Mol. Brain Res. 62:175-186(1998).  
DR EMBL: AB017168; BAA35185.1; -.  
DR HSP; P00743; 1CGF

DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR000359; Cys\_knot.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR003645; FOLN.  
DR InterPro; IPR001791; Laminin\_G.  
DR InterPro; IPR001611; LRR.  
DR InterPro; IPR000483; LRR\_Cterm.  
DR InterPro; IPR000372; LRR\_Nterm.  
DR InterPro; IPR003592; LRR\_out.  
DR InterPro; IPR003591; LRR\_Typ.  
DR Pfam; PF00008; EGF; 9.  
DR Pfam; PF00054; laminin\_G; 1.  
DR Pfam; PF00560; LRR; 17.  
DR Pfam; PF01463; LRRCT; 4.  
DR Pfam; PF01462; LRRNT; 4.  
DR SMART; SM00041; CT; 1.  
DR SMART; SM00179; EGF\_Ca; 2.  
DR SMART; SM00001; EGF\_like; 7.  
DR SMART; SM00274; FOLN; 2.  
DR SMART; SM00282; LamG; 1.  
DR SMART; SM00370; LRR; 6.  
DR SMART; SM00082; LRRCT; 4.  
DR SMART; SM00013; LRRNT; 4.  
DR SMART; SM00369; LRR\_Typ; 8.  
DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_2.  
DR PROSITE; PS01185; CTCK\_1; UNKNOWN\_1.  
DR PROSITE; PS01225; CTCK\_2; 1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_9.  
DR PROSITE; PS01186; EGF\_2; 7.  
DR PROSITE; PS01187; EGF\_Ca; 2.  
KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.  
SQ SEQUENCE 1529 AA; 169866 MW; 5D19CC5E7FD461BA CRC64;

Query Match 16.9%; Score 336; DB 4; Length 1529;  
Best Local Similarity 26.0%; Pred. No. 1.9e-15;  
Matches 105; Conservative 61; Mismatches 120; Indels 118; Gaps 12;

QY 74 CFFGQCYSRVVHCSDLGTSVPTNPFDT-----RMLDL 108

DB 273 CAACTCSNNIVDCRGKGLTEIPTNLP-ETITEIRLEQNTIKVPPGAFSPYKKLRIDL 331

QY 109 QNNKIKKENDFKGLTSLYLILNNKLTKEHPKAFLLTKKRLYLSHNQLSEIPLNL 168

DB 332 SNNQISELAPDAFQGLRSLNSLVYGNKITEPKSLFGLSLQLLLNANKINCLRVDA 391

QY 169 PKSLAELR---IHENKVKIKQDTFGMNAHLVLEMSANP-----LDNNGIE 212

DB 392 FQDLNLLSLYDNKLTQIAKGTSPPLRAITQTHLAQNPFICDHLKWLADYLTNP 451

QY 213 -----PGA----- 215

DB 452 TSGARCTSPRIANRRIQIKSKFRCSAKEQYFIPGTYRSLSGDCFADLACPEKCR 511

QY 216 FGVTVFHIRIAEAKLTSPKGLPPTLELHLDYKNTISTVELED-FKRYKELQRLGLGN 274

DB 512 CGSTTV---DCSNQKLNKIPHIPOYTAELNNNEFTVLEATGIFKLPOLRKINFSNN 568

QY 275 KITDIENGLANIPRVRIHLENNKLK----KIPSGPELKYLIIFLHNSIARVGNVD 330

DB 569 KITDIEGAFEGACSGVNEILLTSNRLNVQHKMFKGLESKTL---MLRSNRITCVGNS 625

QY 331 FCPYTPKMKSLYSALISLFPNPKVWENQAPATFRCVLSRMVQL 374

DB 626 F-----IGLSVRLSLYDNOIT--TVAPGAFDTLHSLSTLN 661

RESULT 16

Q9DE36  
ID Q9DE36 PRELIMINARY; PRT; 1512 AA.  
AC Q9DE36;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE SLIT2.  
GN SLIT2.  
OS Brachydanio rerio (Zebrafish) (Zebra danio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Osteichthyes; Cypriniformes;  
OC Actinopterygii; Neopterygii; Teleostei; Vostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MICHIGAN;  
RA Yeo S.Y.; Okamoto H.;  
RT "zebrafish slit2 homolog."  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF210321; AAG36773.1; -.  
DR HSP; P00740; 1EDM.  
DR ZFIN; ZDB-GENE-010306-3; slit2.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR000359; Cys\_knot.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR001438; EGF\_II.  
DR InterPro; IPR003645; FOLN.  
DR InterPro; IPR002049; Laminin\_EGF.  
DR InterPro; IPR001791; Laminin\_G.  
DR InterPro; IPR001611; LRR.  
DR InterPro; IPR000483; LRR\_Cterm.  
DR InterPro; IPR000372; LRR\_Nterm.  
DR InterPro; IPR003592; LRR\_out.  
DR InterPro; IPR003591; LRR\_Typ.  
DR Pfam; PF00008; EGF; 9.  
DR Pfam; PF00054; laminin\_G; 1.  
DR Pfam; PF00560; LRR; 18.  
DR Pfam; PF01463; LRRCT; 4.  
DR Pfam; PF01462; LRRNT; 4.  
DR PRINTS; PR00010; EGF\_BLOOD.  
DR PRINTS; PR00011; EGF\_LAMININ.  
DR PRINTS; PR00019; LEURICHRPT.  
DR SMART; SM00041; CT; 1.  
DR SMART; SM00181; EGF; 9.  
DR SMART; SM00179; EGF\_Ca; 9.  
DR SMART; SM00001; EGF\_like; 6.  
DR SMART; SM00274; FOLN; 2.  
DR SMART; SM00282; LamG; 1.  
DR SMART; SM00370; LRR; 14.  
DR SMART; SM00082; LRRCT; 4.  
DR SMART; SM00013; LRRNT; 4.  
DR SMART; SM00369; LRR\_Typ; 17.  
DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE; PS01185; CTCK\_1; UNKNOWN\_1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_9.  
DR PROSITE; PS01186; EGF\_2; 8.  
DR PROSITE; PS01187; EGF\_Ca; 2.  
SQ SEQUENCE 1512 AA; 166669 MW; 60888C0AF0C3D630 CRC64;

Query Match 16.8%; Score 335; DB 13; Length 1512;  
Best Local Similarity 27.1%; Pred. No. 2.2e-15;  
Matches 110; Conservative 61; Mismatches 129; Indels 106; Gaps 12;

QY 61 PRSHFFPDLFPMCGCOCYSRVVHCSDLGTSVPTNPFDT----- 103

DB 253 PQSHSCSVL--OCPELCTCSNNVDCRGKGLTEIPTNLP-ETITEIRLEQNSIKIIPAG 309

QY 104 -----RMLDLQNNKIKKENDFKGLTSLYLILNNKLTKEHPKAFLLTKKRLYL 155

DB 310 AFAPYKRLRRIDLNNQITELASDSFQGLRSLNSLVYGNKITEPKSLFGLSLQLLL 369

[illegible]







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DR EMBL; AY046070; AAL02123.1; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR Pfam; PF00008; EGF_9.
DR Pfam; PF00054; laminin_G; 1.
DR Pfam; PF00560; LRR; 17.
DR Pfam; PF01462; LRRCT; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_2.
DR PROSITE; PS01185; CTCK_1; UNKNOWN_1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_9.
DR PROSITE; PS01186; EGF_2; UNKNOWN_7.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_2.
SQ SEQUENCE 1530 AA; 170101 MW; AB4C4650CBA4218C CRC64;

Query Match 16.68; Score 331; DB 13; Length 1530;
Best Local Similarity 26.88; Pred. No. 4.3e-15;
Matches 106; Conservative 60; Mismatches 120; Indels 110; Gaps 12;

Qy 74 CPFGQCYSRVVHCSDGLTSVPTNIPDFT-----RMLDL 108
Db 282 CPAACTCSNNIVDCRGKGLTEIPTNLP-ETITEIRLEQNTIKVIPPGAFSPYKLLRRIDL 340

Qy 109 QNNKIKEIKENDFKGLTSLYGLILNKKLTAKIHPKAFITTKLRLRLYLHNSQLSEIPLNL 168
Db 341 SNNQISEIADAFQGLSLNSLVYGNKITEPKLFEGLFSQLLLNANKINCLRVDS 400

Qy 169 PKSLAELR---IHENKVKKTKQDTFKGMNALHVLMSANP-----LDNNGIE 212
Db 401 FQDLHNLNLLSYDNKLTQIAKGTSPFLRAIQTLMHQAQNPFCIDCHLKLADYLHTNP 460

Qy 213 -PGA-----FEQVTVFH 223
Db 461 TSGARCTSPRLANKRIGQIKSKFRCSGTEDYRSKLSGDCFADLACPEKCRCEGTV-- 518

Qy 224 IRIAEAKLTSVPKGLPPTLLLEHLHDYNNKISTVELED-FKRYKELQRLGLGNKNTIDENG 282
Db 519 -DCSNQKLTKEIPDHPQYTAELRLNNEFTVLEATGIFKKLPOLRKINLSNNKITDIEG 577

Qy 283 SLANIPRVREIHLNENKILK-----KIPSGLPKYLQIIFLHNSIARVGVNDFCPTVPKM 338
Db 578 AFEAGANGVNEILLTSNRLENVQHKMFKEKLEKLTPL---MLRSNHISCVNNDSTGL---- 630

Qy 339 KKSLSAISLFFNNPVKYWEMOPATFRCVLSRMSVOL 374
Db 631 --SSVRLLSLYDNQIT--TVAPGAFDTLHLSLSTLNL 662

RESULT 23
O95710 PRELIMINARY; PRT; 1521 AA.
AC O95710;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Neurogenic extracellular SLIT protein SLIT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY, AND BRAIN;
RX MEDLINE=99279238; PubMed=10349621;
RA Holmes G.P., Negus K., Burridge L., Raman S., Algar E., Yamada T.,

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RA Little M.H.;
RT "Distinct but overlapping expression patterns of two vertebrate slit
RT homologs implies functional roles in CNS development and
RT organogenesis.";
RL Mech. Dev. 79:57-72(1998).
DR EMBL; AF055585; AAD04309.1; -.
DR HSP; P00743; ICCF.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003592; LRR_out.
DR Pfam; PF00008; EGF; 9.
DR Pfam; PF00054; laminin_G; 1.
DR Pfam; PF00560; LRR; 17.
DR Pfam; PF01463; LRRCT; 4.
DR SMART; SM00041; CT; 1.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00001; EGF_Like; 7.
DR SMART; SM00274; FOLN; 2.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00370; LRR; 5.
DR SMART; SM00082; LRRCT; 4.
DR SMART; SM00013; LRRNT; 4.
DR SMART; SM00369; LRR_TYP; 8.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_2.
DR PROSITE; PS01185; CTCK_1; UNKNOWN_1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_9.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS01187; EGF_CA; 2.
KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
SQ SEQUENCE 1521 AA; 168947 MW; COSA0DFD7D78C48C9 CRC64;

Query Match 16.5%; Score 329; DB 4; Length 1521;
Best Local Similarity 25.7%; Pred. No. 5.9e-15;
Matches 101; Conservative 64; Mismatches 124; Indels 104; Gaps 11;

Qy 74 CPFGQCYSRVVHCSDGLTSVPTNIPDFT-----RMLDL 108
Db 273 CPAACTCSNNIVDCRGKGLTEIPTNLP-ETITEIRLEQNTIKVIPPGAFSPYKLLRRIDL 331

Qy 109 QNNKIKEIKENDFKGLTSLYGLILNKKLTAKIHPKAFITTKLRLRLYLHNSQLSEIPLNL 168
Db 332 SNNQISEIADAFQGLSLNSLVYGNKITEPKLFEGLFSQLLLNANKINCLRVDA 391

Qy 169 PKSLAELR---IHENKVKKTKQDTFKGMNALHVLMSANP-----LDNNGIE 212
Db 392 FQDLHNLNLLSYDNKLTQIAKGTSPFLRAIQTLMHQAQNPFCIDCHLKLADYLHTNP 451

Qy 213 -PGA-----FEQVTVFH 223
Db 452 TSGARCTSPRLANKRIGQIKSKFRCSGTEDYRSKLSGDCFADLACPEKCRCEGTV-- 509

Qy 224 IRIAEAKLTSVPKGLPPTLLLEHLHDYNNKISTVELED-FKRYKELQRLGLGNKNTIDENG 282
Db 510 -DCSNQKLTKEIPDHPQYTAELRLNNEFTVLEATGIFKKLPOLRKINLSNNKITDIEG 568

Qy 283 SLANIPRVREIHLNENKILKIPSGL-PEKYLQIIFLHNSIARVGVNDFCPTVPKMKS 341
Db 569 AFEAGANGVNEILLTSNRLENVQHKMFKEKLEKPLQNLMLRSNRTITCVGNDSF-----IGLS 622

Qy 342 LYSATSLFNNPVKYWEMOPATFRCVLSRMSVOL 374
Db 623 SVRMLSLYDNQIT--TVAPGAFDTLHLSLSTLNL 653

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RESULT 24
O9WB5 PRELIMINARY; PRT; 1531 AA.
ID Q9WB5
AC Q9WB5
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SLIT1.
CN SLIT1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SWISS WEBSTER/ICR;
RX MEDLINE=93365246; PubMed=10433822;
RA Yuan W., Zhou L., Chen J.H., Wu J.Y., Rao Y., Ornitz D.M.;
RT "The mouse SLIT family: secreted ligands for ROBO expressed in
RL Dev. Biol. 212:290-306(1999).
DR EMBL; AF144627; AA044758.1; -.
DR HSP; P00743; ICCF.
DR MGD; MGI:1315203; Slit1.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR003645; FOLN.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00008; EGF; 9.
DR Pfam; PF00054; laminin_G; 1.
DR Pfam; PF00560; LRR; 19.
DR Pfam; PF01463; LRRCT; 4.
DR PRINTS; PR00010; EGFBL00D.
DR SMART; SM00041; CT; 1.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00001; EGF_like; 7.
DR SMART; SM00274; FOLN; 2.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00370; LRR; 3.
DR SMART; SM00013; LRRNT; 4.
DR SMART; SM00369; LRR_TYP; 10.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_2.
DR PROSITE; PS01185; CTCK_1; UNKNOWN_1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_9.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS01187; EGF_CA; 2.
KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
SQ SEQUENCE 1531 AA; 167546 MW; F7D09AA6693A4F30 CRC64;

Query Match 16.5%; Score 329; DB 11; Length 1531;
Best Local Similarity 25.5%; Pred. No. 6e-15;
Matches 100; Conservative 62; Mismatches 116; Indels 114; Gaps 10;

QY 74 CPFCQCYSRVVHCDLGLTVPNTIPFDT-----RMLDL 108
| | | | | | | | | | | | | | | | | | | | |
Db 282 CPAMCSCSSGIVDCRGKGLTAIPANLP-ETWTEIRLELNGIKSIPTGCAFSYRKLRRIDL 340
| | | | | | | | | | | | | | | | | | | | |
QY 109 QNNKIKEIKENDFKLTLGLIINNNKLTIIHPKAPLTTKKLRLRYLSNQLSEI---P 165
| | | | | | | | | | | | | | | | | | | | |

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Db 73 CPRVCSCTGLNVDCHSHRGLTSVPRKISADVERLELQGNLTVIYETDFQRLTKLRMLQLT 132
QY 134 NNLTKIHPKAFITTKLRRLYLNSHNSLSEPLNL---PKSLAELRHENKVKKIQKDTF 190
Db 133 DQIHTIERNFQDVLUSLRNLRNLUKAIPEFNVTSASLLRLDISNNVITTVGRVF 192
QY 191 KGMALHVLNSANPLDNGI---EPGAFEGVTVFHI----- 224
Db 193 KGAQSLRSIQ-----LDNNQITCLDEHAFGLVELEILTNNNLTSILPHNIFGGLRLR 247
QY 225 -----RIA----- 227
Db 248 ALRLSDNPFACDCHLSWLSRSLRSATRLAPYTRCQSPSQLKQNVADLHDQEFKCSGLTE 307
QY 228 -----EAKLTSVPKGLPPTLLELHLDYKNKISTVELEDFK 261
Db 308 HAPMECGAENSCHPCRCADGIVCREKSLTSVPVTPDDTTLELRLEQNFITELPPKSF 367
QY 262 RYKQLRLGLGNKTKITDIENGLANIPRVREIHLNENKLNKIPSGL-PELKYLQIIFLHS 320
Db 368 SFRRRLRIDLSNNISRIHTADLSQLKQLTTLVLYGNKIKRDLPSGVKGLGSLQLLLNA 427
QY 321 NSIARVGVNDPCPTVPKMKSLY---SAISLNNPVKYWMQPATFRCVLSRMSVOL 374
Db 428 NEISCIRKDAF-----RDLHLSLSLLYDNNITQ---SLANGTFDAMKSIKTVHL 473

RESULT 27
Q9WVB4 PRELIMINARY; PRT; 1523 AA.
AC Q9WVB4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SLIT3 (Fragment).
GN SLIT3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SWISS WEBSTER/ICR;
RX MEDLINE=95365246; PubMed=10433822;
RA Yuan W., Zhou L., Chen J.H., Wu J.Y., Rao Y., Ornitz D.M.;
RT "The mouse Slit family: secreted ligands for ROBO expressed in
RL patterns that suggest a role in morphogenesis and axon guidance.";
RL Dev. Biol. 212:290-306(1999).
DR EMBL; AF144629; AAD44760.1; -.
DR HSSP; P01132; IEGF.
DR MGD; MGI:1315202; Slit3.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF-2.
DR InterPro; IPR001881; EGF-Ca.
DR InterPro; IPR001438; EGF-II.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00008; EGF; 9.
DR Pfam; PF00054; laminin_G; 1.
DR Pfam; PF00560; LRR; 19.
DR Pfam; PF01463; LRRCT; 4.
DR Pfam; PF01462; LRRNT; 4.
DR PRINTS; PR00010; EGFBLLOOD.
DR PRINTS; PR00011; EGFFLAMININ.
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DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00041; CT; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 5.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00370; LRR; 7.
DR SMART; SM00082; LRRCT; 4.
DR SMART; SM00013; LRRNT; 4.
DR SMART; SM00369; LRR_TYP; 7.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_2.
DR PROSITE; PS01185; CTCK_1; UNKNOWN_1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_9.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS01187; EGF_CA; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
FT NON_TER 1523 1523
SQ SEQUENCE 1523 AA; 167711 MW; F43A3F3E016C4BFC CRC64;

Query Match 16.3%; Score 325; DB 11; Length 1523;
Best Local Similarity 25.4%; Pred. No. 1.1e-14;
Matches 100; Conservative 59; Mismatches 111; Indels 124; Gaps 9;

QY 74 CPGCCQCYSRVHCHSDGLTSTVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
Db 34 CPTKCTCSAASVDCHGLGLRAVPRGIPRPAERLDLRNITRTKMDFAGLNLRVHLE 93
QY 134 NNLTKIHPKAFITTKLRRLYLNSHNSLSEPLNLPSK---LAELRIHENKVKKIQKDTF 190
Db 94 DNOVSTIERGAFQDLKQLERLRLNKNKQLVPELLFQSTPKLTRDLSENIOGIPRKAF 153
QY 191 KGMALHVLNSANPLDNG---IEGAREG-----VTFP----- 222
Db 154 RGTGVKNLQ-----LDNNHISCIEDGAFRALRDLLEILTNNNNISRLVTSFNHMPKIR 208
QY 223 -----HIR-----IAEK----- 230
Db 209 TLRHSHNLYCDCHLAWLSDWLRLQRRTIGOTLCMAPVHLRGFSVADVOKKEVCPGPHS 268
QY 231 -----LTSVPKGLPPTLLELHLDYKNKISTVELEDFK 261
Db 269 EAPACNANSLSCPSACSCSNIVDCRGKGLTEIPANLPEGIVIRLEQNSIKSIPAGATF 328
QY 262 RYKELORLGLGNKTKITDIENGLANIPRVREIHLNENKLNKIPSGLPE-LKYLQIIFLHS 320
Db 329 QYKLRIDISKNQISDIAPDAFQGLKSLTSLVLYGNKITEIPKGLDGLVSLQLLLNA 388
QY 321 NSIARVGVNDPCPTVPKMKSLYSALSFNPNVK 354
Db 389 NKINCLRVNTF-----QDLQNLNLLSYDNKLQ 416

RESULT 28
Q9V7F8 PRELIMINARY; PRT; 1480 AA.
AC Q9V7F8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE SLI protein.
GN SLI OR CG8355.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
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RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers J.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Bayandale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.I., Benos P.V., Berhan B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadenot L.B., Davies P.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foslter C., Gabrieli A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RA "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003809; AAF58098.1; -.  
 DR HSP: P00740; IEDM.  
 DR FlyBase: FBgn003425; sli.  
 DR InterPro: IPR000152; Asx\_hydroxyl.  
 DR InterPro: IPR000359; Cys\_knot.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR000742; EGF\_2.  
 DR InterPro: IPR001881; EGF\_Ca.  
 DR InterPro: IPR002049; Laminin\_EGF.  
 DR InterPro: IPR001791; Laminin\_G.  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR000483; LRR\_Cterm.  
 DR InterPro: IPR000372; LRR\_Nterm.  
 DR InterPro: IPR003592; LRR\_Out.  
 DR InterPro: IPR003591; LRR\_typ.  
 DR Pfam: PF00007; Cys\_knot; 1.  
 DR Pfam: PF00008; EGF; 7.  
 DR Pfam: PF00054; laminin\_G; 1.  
 DR Pfam: PF00560; LRR; 16.  
 DR Pfam: PF01463; LRRCT; 4.  
 DR Pfam: PF01462; LRRNT; 4.  
 DR PRINTS: PR00011; EGF\_LAMININ.  
 DR PRINTS: PR00019; LEURICHRPT.  
 DR SMART: SM00041; CT; 1.  
 DR SMART: SM00179; EGF\_CA; 2.  
 DR SMART: SM00001; EGF\_like; 5.  
 DR SMART: SM00282; LamG; 1.  
 DR SMART: SM00370; LRR; 4.  
 DR SMART: SM00082; LRRCT; 4.  
 DR SMART: SM00013; LRRNT; 4.  
 DR SMART: SM00369; LRR\_Typ; 9.  
 DR PROSITE: PS00010; ASX\_HYDROXYL; 3.  
 DR PROSITE: PS01185; CTCK\_1; 1.  
 DR PROSITE: PS01225; CTCK\_2; 2.  
 DR PROSITE: PS00022; EGF\_1; 14.  
 DR PROSITE: PS01186; EGF\_2; 10.  
 DR PROSITE: PS01187; EGF\_CA; 1.

KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.  
 SQ SEQUENCE 1480 AA; 165888 MW; F456BC617D8453ED CRC64;  
 Query Match 16.3%; Score 324; DB 5; Length 1480;  
 Best Local Similarity 25.8%; Pred. No. 1.3e-14;  
 Matches 101; Conservative 63; Mismatches 123; Indels 104; Gaps 9;  
 QY 74 CPFGQCQYRVVHCSDGLTSTVPTNPEDT-----RMLDLQ 109  
 DB 73 CPVVCSTGLNVDCSHRGTSVPRKISADVERLEQGNLTIVYETDFQRLTKRLMLQLT 132  
 QY 110 NKKIETENDFKGLTSLYGLILNKKLTHTKRAFLTKLRLLYLSHNQLSEIPLNLP 169  
 DB 133 DQNIHTIERNSPQDLVSLERLIDISNNVTTVGRRVFKGAQSLRSLOLDNNQITCLDEHAF 192  
 QY 170 KSLAELRI---HENKVKIKQDKTFKGMALHVLMSANPL----- 206  
 DB 193 KGLVELEILTLNNNLTSLPHNIFGGLRLRALRLSDNPFACDCHLSWLSRFLRSATRLA 252  
 QY 207 -----DNNGLEPGA-----FGVTVFHIRI 226  
 DB 253 PYTRCQSPSQLKQSNVADLHDQEFKCSGLTEHAPMECGAENSCHPCCRADGI----VDC 308  
 QY 227 AEAKLTSPKGLPPTLLELHLDYNKISTVELEDKRYRELQRLGLGNKNTIDENGSLAN 286  
 DB 309 RKKSITSPVPTLPDDTTLEQLQNFITELPKPSFSFRLRLRIDLSNNNISRIADHLSG 368  
 QY 287 IPRVREIHLENNKLLKIPSGL-PELKYLOITFLHSNSIARVGVNDFCTVPKMKKSY-- 343  
 DB 369 LKQLTTLVLYGNKIKDLPSPGVFKGLSLOLLLNANEISCTRKDAF-----RDLHSL 420  
 QY 344 SAISLFPNPVKYWMQPATFRCVLSRMSVOL 374  
 DB 421 SLLSYDNNIQ--SLANGTFDAMKSIKTVHL 449  
 RESULT 29  
 O88280 PRELIMINARY; PRT: 1523 AA.  
 AC O88280;  
 DT 01-NOV-1998 (Tremblrel. 08, Created)  
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE MEGF5.  
 GN MEGF5.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;  
 RX MEDLINE=98360089; PubMed=9693030;  
 RA Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;  
 RT "Identification of high-molecular-weight proteins with multiple EGF-  
 RT like motifs by motif-trap screening.";  
 RL Genomics 51:27-34(1998).  
 DR EMBL: AB011531; BAA32461.1; -.  
 DR HSP: P01132; IEGF.  
 DR InterPro: IPR000152; Asx\_hydroxyl.  
 DR InterPro: IPR000359; Cys\_knot.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR000742; EGF\_2.  
 DR InterPro: IPR001881; EGF\_Ca.  
 DR InterPro: IPR002400; GF\_cysknot.  
 DR InterPro: IPR001791; Laminin\_G.  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR000483; LRR\_Cterm.  
 DR InterPro: IPR000372; LRR\_Nterm.  
 DR InterPro: IPR003592; LRR\_Out.  
 DR InterPro: IPR003591; LRR\_typ.  
 DR Pfam: PF00008; EGF; 9.  
 DR Pfam: PF00054; laminin\_G; 1.

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DR Pfam: PF00560; LRR; 19.
DR Pfam: PF01463; LRRCT; 4.
DR Pfam: PF01462; LRRNT; 4.
DR PRINTS: PR00438; GFCYSKNOT.
DR SMART: SM00041; CT; 1.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00001; EGF_Like; 8.
DR SMART: SM00282; LamG; 1.
DR SMART: SM00370; LRR; 5.
DR SMART: SM00082; LRRCT; 4.
DR SMART: SM00013; LRRNT; 4.
DR SMART: SM00369; LRR_TTP; 9.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_2.
DR PROSITE: PS01185; CTCK_1; UNKNOWN_1.
DR PROSITE: PS01225; CTCK_2; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_9.
DR PROSITE: PS01186; EGF_2; 7.
DR PROSITE: PS01187; EGF_CA; 2.
DR Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
KW SEQUENCE 1523 AA; 167767 MW; 6CE1B7AF9244478E CRC64;

Query Match 16.3%; Score 324; DB 11; Length 1523;
Best Local Similarity 25.4%; Pred. No. 1.3e-14;
Matches 100; Conservative 59; Mismatches 111; Indels 124; Gaps 9;

Qy 74 CPFGCCYSRVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKETKENDFKGLTSLYGLILN 133
Dy 34 CPTKCTCSAASVDCGHLGLRAVPRGIPRNERLDLDRNTRITKMDFTGLKNLRVLALE 93

Qy 134 NKKITKHPKAFITTKLRLYLHSHNLSLSEIPNLPKS---LAELRIHENKVKKIQKDTF 190
Dy 94 DNQSVTERGAFQDLKQLERLRLNKNLQVPELLFQSTPKLTLDELSENIQIIPKAF 153

Qy 191 KGMALHVLANSAPLDNNG---LEPAFEG-----VTVF----- 222
Dy 154 RGVTVGNLQ-----LDNNHISCIEDGAFRALRDLLEILTNNNNISRLVTSFNHMPKIR 208

Qy 223 -----HIR---IAEAK----- 230
Dy 209 TLRHSHLYCDCHLWLSDWLRORRTIGQFTLCMAVPHLRGVSADVQKVEYVCPGPHS 268

Qy 231 -----LTSVPKGLPPTLLEHLHDYNNKISTVELEDFK 261
Dy 269 EAPACNANSLSCPSACSNNIVDCRGKGLTEIPANLPEGIVEIRLEQNSIKSPAGAFI 328

Qy 262 RYKELRLGLGNKNTDIENGSLANIPRVREIHLNKKIKIPSGLPE-LKYLIQIFLHS 320
Dy 329 QYKKLRIDISKNQISDIADPAFGKLSLTSVLYGNKITEIPKGLFDGLVSLQLLLNA 388

Qy 321 NSIARVGVNDFCTVPRMKKSLYSALSFNNPVK 354
Dy 389 NKINCLRVNTE-----QDLQNLNLSLYDNKLQ 416

RESULT 30
O88279 PRELIMINARY; PRT; 1531 AA.
AC O88279;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MEGF4.
GN MEGF4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE=98360089; PubMed=9693030;
RA Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;
RT *Identification of high-molecular-weight proteins with multiple EGF-
```

```

RT like motifs by motif-trap screening.";
RL Genomics 51:27-34(1998).
DR EMBL: AB011530; BAA32460.1; -.
DR HSSP: P00743; IAPO.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000359; Cys_knot.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_CA.
DR InterPro: IPR001438; EGF_II.
DR InterPro: IPR003645; FOLN.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Nterm.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR003592; LRR_out.
DR InterPro: IPR003591; LRR_typ.
DR Pfam: PF00008; EGF; 9.
DR Pfam: PF00054; laminin_G; 1.
DR Pfam: PF00560; LRR; 19.
DR Pfam: PF01463; LRRCT; 4.
DR Pfam: PF01462; LRRNT; 4.
DR PRINTS: PR00010; EGF_BLOOD.
DR SMART: SM00041; CT; 1.
DR SMART: SM00179; EGF_CA; 2.
DR SMART: SM00001; EGF_Like; 7.
DR SMART: SM00274; FOLN; 3.
DR SMART: SM00282; LamG; 1.
DR SMART: SM00370; LRR; 3.
DR SMART: SM00082; LRRCT; 4.
DR SMART: SM00013; LRRNT; 4.
DR SMART: SM00369; LRR_TTP; 10.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_2.
DR PROSITE: PS01185; CTCK_1; UNKNOWN_1.
DR PROSITE: PS01225; CTCK_2; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_9.
DR PROSITE: PS01186; EGF_2; 8.
DR PROSITE: PS01187; EGF_CA; 2.
KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
SQ SEQUENCE 1531 AA; 167497 MW; DFC4B60CCBC5529A CRC64;

Query Match 16.2%; Score 323; DB 11; Length 1531;
Best Local Similarity 25.0%; Pred. No. 1.6e-14;
Matches 98; Conservative 64; Mismatches 116; Indels 114; Gaps 10;

Qy 74 CPFGCCYSRVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKETKENDFKGLTSLYGLILN 108
Dy 282 CPAMCSCSNGIVDCRGKGLTAIPANLP-ETMTETIRLELNGIKSIPPGAFSPYKLRIDL 340

Qy 109 QNNKIKEIKENDFKGLTSLYGLITLNNKLTIKHPKAFITTKLRLYLHSHNLSLSEIPNL 165
Dy 341 SNNQIAETAPDAFQGLRSLNSLVYGNKITDLPGRVFGGLYTLQLLLNANKINCIRPDA 400

Qy 166 LNLPSLAELRIHENKVKKIQKDTFKGMNALHVLANSAP-----LDNNGIE 212
Dy 401 FQDLQNLNLSLYDNKIQSLAKGTTSLRAIQTLLHAQNPFFCDCLNKLWDLFLRTNPTE 460

Qy 213 -PGA-----PEGVTVFH----- 223
Dy 461 TTGARCASPRRLANKRIGQIKSKKFCRSKAEQYIFPGTEDIHLNLSCTSDVACPCHKCR 520

Qy 224 ---IRIAEAKLTSPKGLPPTLLEHLHDYNNKISTVELED-FKRYKELQRLGLGNKITDI 279
Dy 521 ASVVECSGLKSLKIPERIPQSTTELNNNEISILEATGLFKLSHLKINLSNNKVSIEI 580

Qy 280 ENGLANIPRVREIHLNKKIKIPSGL-PELKYLIQIIFLHNSIARVGVNDFCTVPMK 338
Dy 581 EDGTFFEGATSVSELHLTANQLESVRSRGMDGLDGLRTLMLRNNRISCIHNSDFTGLNRVR 640

Qy 339 KKSLEY-----SAISLFNNP 352
Dy 641 LLSLYDNHITTPSPGAFDTLQALSTLNLLANP 672
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## RESULT 31

Q8WVZ2 PRELIMINARY; PRT; 798 AA.  
 AC Q8WVZ2  
 ID Q8WVZ2  
 DT 01-MAR-2002 (Tremblrel. 20, Created)  
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE SLIT1 isoform B (Fragment).  
 GN SLIT1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Teasdale R.D., Rumballe B., Georgas K., Yamada T., Little M.H.;  
 RT "Conserved modularity, size and potential for alternate splicing in  
 RT all three human Slit genes".  
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY029183; AAK31796.1; -.  
 DR Flybase; FBgn0003425; slit.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR000483; LRR\_Cterm.  
 DR InterPro; IPR000372; LRR\_Nterm.  
 DR InterPro; IPR003592; LRR\_Out.  
 DR InterPro; IPR003591; LRR\_Typ.  
 DR Pfam; PF00560; LRR; 15.  
 DR Pfam; PF01463; LRRCT; 3.  
 DR Pfam; PF01462; LRRNT; 4.  
 DR PRINTS; PR00019; LEURICHRPT.  
 DR SMART; SM00370; LRR; 11.  
 DR SMART; SM00082; LRRCT; 3.  
 DR SMART; SM00013; LRRNT; 4.  
 DR SMART; SM00369; LRR\_TYP; 16.  
 FT NON\_TER 1  
 FT 798  
 SQ SEQUENCE 798 AA; 88906 MW; 1A9094A414BABD04 CRC64;

Query Match 16.1%; Score 320; DB 4; Length 798;  
 Best Local Similarity 24.7%; Pred. No. 1.2e-14;  
 Matches 100; Conservative 69; Mismatches 124; Indels 112; Gaps 11;

QY 74 CPFGCCQCYSRVHCSDGLTSLVPTNIP----- 100  
 DB 265 CPAMCTCSNGIVDCRGKLLTAIFAULPETWETIRLELNGIKSIIPGAFSPYKLRIRPL 324  
 QY 101 -FDTPLMLDQNNKTIKENDFKGLTSLYGLIILNNKLTIKHPKAFITTKKRLRLSHN 159  
 DB 325 SFCSPCDLSNNQIAETAPDAFQGLRSLSLVYGNKTTDLPRGVGGLYTLQLLLNAN 384  
 QY 160 QLSI-----PLNPKSLAELRIHENKVKIKOKDFKGMNALHVLMSANP----- 205  
 DB 385 KINCIRPDAFQDLQNLSSLSDYDNKIQSLAKGTTLSLRAIOTLHLAQNPFICDCNLKWL 444  
 QY 206 --LDNNGIE-----PGAFE-----GV 219  
 DB 445 DFLTNPIETSGARCASPRLANKRIGQIKSKKPRCSAKQYPIPTEDYQLNSECNSDV 504  
 QY 220 TVFH-----TRIAEAKLTSVPKGLPPTLLLEHLHDYNNKISTVELED-FKRYKELQRLG 270  
 DB 505 VCPHKRCLEANVVCSSLKTKIPERIPQSTAEALRNNEISILEATGMFKLTHLKIN 564  
 QY 271 LGNNKITYDIENGSLANIPRVRETHLENNKLUKIPSGL-PELKYLIQIFLHNSIARGVN 329  
 DB 565 LSNKVKSEIEDGAFEGAAVSSELHLTANQLSEIRSGMFRGLDRLTILMRNNRISCIH-N 623  
 QY 330 DFECTVPKMKSLYSATSLNPNPKYKWEOPATFRCVLSRMSVOL 374  
 DB 624 DSFTGLNRV-----LLSLYDNOIT--TVSPGAFDTLQSLSTLNL 661

## RESULT 32

Q9XYV4

Q9XYV4 PRELIMINARY; PRT; 1504 AA.  
 AC Q9XYV4;  
 DT 01-NOV-1999 (Tremblrel. 12, Created)  
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE SLIT protein  
 GN SLI OR SLIR OR CG8355.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=99200390; PubMed=10102267;  
 RA Kidd T., Bland K.S., Goodman C.S.;  
 RT "Slit is the midline repellent for the robo receptor in Drosophila.";  
 RL Cell 96:785-794(1999).  
 DR EMBL; AF126540; AAD26567.1; -.  
 DR HSSP; P00740; IEDM.  
 DR Flybase; FBgn0003425; slit.  
 DR InterPro; IPR000152; Asx\_Hydroxyl.  
 DR InterPro; IPR000359; Cys\_knot.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_CA.  
 DR InterPro; IPR002049; Laminin\_EGF.  
 DR InterPro; IPR001791; Laminin\_G.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR000483; LRR\_Cterm.  
 DR InterPro; IPR000372; LRR\_Nterm.  
 DR InterPro; IPR003592; LRR\_Out.  
 DR InterPro; IPR003591; LRR\_Typ.  
 DR Pfam; PF00007; Cys\_knot; 1.  
 DR Pfam; PF00008; EGF; 7.  
 DR Pfam; PF00054; laminin\_G; 1.  
 DR Pfam; PF00560; LRR; 17.  
 DR Pfam; PF01463; LRRCT; 4.  
 DR Pfam; PF01462; LRRNT; 4.  
 DR PRINTS; PR00011; EGF\_LAMININ.  
 DR PRINTS; PR00019; LEURICHRPT.  
 DR SMART; SM00041; CT; 1.  
 DR SMART; SM00179; EGF\_CA; 2.  
 DR SMART; SM00001; EGF\_like; 5.  
 DR SMART; SM00282; LamG; 1.  
 DR SMART; SM00370; LRR; 4.  
 DR SMART; SM00082; LRRCT; 4.  
 DR SMART; SM00013; LRRNT; 4.  
 DR SMART; SM00369; LRR\_TYP; 9.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_3.  
 DR PROSITE; PS01185; CTCK\_1; 1.  
 DR PROSITE; PS01225; CTCK\_2; 1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_7.  
 DR PROSITE; PS01186; EGF\_2; 5.  
 DR PROSITE; PS01187; EGF\_CA; 2.  
 KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.  
 SQ SEQUENCE 1504 AA; 168569 MW; A377D3BAACBIC743 CRC64;

Query Match 16.1%; Score 320; DB 5; Length 1504;  
 Best Local Similarity 25.2%; Pred. No. 2.5e-14;  
 Matches 105; Conservative 57; Mismatches 124; Indels 130; Gaps 9;

QY 74 CPFGCCQCYSRVHCSDGLTSLVPTNIPEDTRMLDQNNKIKRKENDFKGTSLYGLIN 133  
 DB 73 CPKVCSCGTGLNVDCSHRGLTSVPKISADVERLEQGNLTVIVETDFQRLTKRLMLQLT 132  
 QY 134 NNKLTIKHPKAFITTKKRLRLYLSHNSQLSEIPLNL---PKSLAELRIHENKVKIKORDTF 190  
 DB 133 DNQHTTIERNFQDLVLSLERLNNRLKAIPENFVTSASLLRLDTSNNVITTVGRVF 192  
 QY 191 KGMNALHVLMSANPLDNNGI---EPGAFEGVTVFHI----- 224  
 DB 193 KGAQSLSIQ-----LDNNQITCLDEHAFKGLGVEILTLNNNLTSLPHNIFGLGLRLR 247





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DR InterPro: IPR003591; LRR_typ.
DR Pfam: PF00008; EGF; 9.
DR Pfam: PF00054; laminin_G; 1.
DR Pfam: PF00560; LRR; 18.
DR Pfam: PF01463; LRRCT; 4.
DR Pfam: PF01463; LRRCT; 4.
DR PRINTS: PR00019; LEURICHRPT.
DR SMART: SM00041; CT; 1.
DR SMART: SM00181; EGF; 9.
DR SMART: SM00179; EGF_CA; 8.
DR SMART: SM00001; EGF_like; 6.
DR SMART: SM00282; LRR; 14.
DR SMART: SM00370; LRR; 14.
DR SMART: SM00082; LRRCT; 4.
DR SMART: SM00013; LRRNT; 4.
DR SMART: SM00369; LRR_TYP; 18.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS01185; CTCK_1; UNKNOWN_1.
DR PROSITE: PS01225; CTCK_2; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_9.
DR PROSITE: PS01186; EGF_2; 7.
DR PROSITE: PS01187; EGF_CA; 2.
SQ SEQUENCE 1515 AA; 166871 MW; 12FD1111277D18D5B CRC64;

Query Match 15.6%; Score 311.5; DB 13; Length 1515;
Best Local Similarity 23.9%; Pred. No. 1e-13;
Matches 94; Conservative 63; Mismatches 114; Indels 123; Gaps 9;

QY 74 CPFGCCYSRVVHCSDGLTSVPTNIPFDTRMLDQNNKIKEIKENDPKGLTSLYGLILN 133
DB 24 CPHKCSGSHVDCGQAFKTPVPGIPRPAERLDLRNNITRTTKMDPAGLKNLRLVHLE 83
QY 134 NKLTKIHPKAPLTKRLRLYLSHNOLSEIPLMKPS---LAEIRIHENKVKIKQDTF 190
DB 84 NNOISVIERGAFEGKQLERIRLNRLNQLVPELLFQSTKLSRLDSENOIQAVPKAF 143
QY 191 KGMNALHVLENSANPLDNGIEGAF----- 216
DB 144 GRITTVNQLQDSNHI---SCIEDGAFRALRDLEILTLNNNITLIPLSSFNHMPKRLTLR 201
QY 217 -----EGVTVF-----HIR----- 225
DB 202 LHSNNLHCDCHLSWLDWRQRGLAFPTQCMAPAHNRGLNVPDQKREVCVETEP 261
QY 226 -----IAEAK-----LTSVPKGLPTLLEHLVDYKNISTVELEDFKRY 263
DB 262 RSCAQTICPACTCNVIVDCRRKGLTEIPANLPEGIVEIRLEQNMKINIPAGAFSTY 321
QY 264 KELQRLGNGNKITDIENGSLANIPRVREIHLNENKLLKTPSLGLPE-LKYLOIIFLHNS 322
DB 322 KKLRIIDLKNOISEIAEDAFSGURSLTSLVYGNKIAEIPKGLFDGLVSLQLLLNANK 381
QY 323 TARYGVNDFCPTVPKMKKSL--YSALSFNPNVK 354
DB 382 INCLRVNTF-----KDLQNLNLSLYDNKLQ 407

RESULT 35
ID 075094 PRELIMINARY; PRT; 1523 AA.
AC 075094;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-AUG-1999 (TREMBLrel. 11, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Slit-3 protein (MEGF5).
GN Slit-3 OR MEGF5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99033071; PubMed=9813312;
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RA InterPro: IPR003591; LRR_typ.
RA Pfam: PF00008; EGF; 9.
RA Pfam: PF00054; laminin_G; 1.
RA Pfam: PF01463; LRRCT; 4.
RA Pfam: PF01463; LRRCT; 4.
RA PRINTS: PR00019; LEURICHRPT.
RA SMART: SM00041; CT; 1.
RA SMART: SM00181; EGF; 9.
RA SMART: SM00179; EGF_CA; 1.
RA SMART: SM00001; EGF_like; 5.
RA SMART: SM00282; LamG; 1.
RA SMART: SM00370; LRR; 4.
RA SMART: SM00082; LRRCT; 4.
RA SMART: SM00013; LRRNT; 4.
RA SMART: SM00369; LRR_TYP; 9.
RA PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_2.
RA PROSITE: PS01185; CTCK_1; UNKNOWN_1.
RA PROSITE: PS01225; CTCK_2; 2.
RA PROSITE: PS00022; EGF_1; UNKNOWN_9.
RA PROSITE: PS01186; EGF_2; 7.
RA PROSITE: PS01187; EGF_CA; 2.
RA PROSITE: PS00290; IG_MHC; UNKNOWN_1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
SQ SEQUENCE 1523 AA; 167684 MW; 52549D41D1D6DBD1 CRC64;

Query Match 15.5%; Score 309; DB 4; Length 1523;
Best Local Similarity 24.9%; Pred. No. 1.6e-13;
Matches 98; Conservative 58; Mismatches 114; Indels 124; Gaps 9;

QY 74 CPFGCCYSRVVHCSDGLTSVPTNIPFDTRMLDQNNKIKEIKENDPKGLTSLYGLILN 133
DB 34 CPTKCTCSAASVDCHGLGRLAVPRGIPRPAERLDLRNNITRTTKMDPAGLKNLRLVHLE 93
QY 134 NKLTKIHPKAPLTKRLRLYLSHNOLSEIPLMKPS---LAEIRIHENKVKIKQDTF 190
DB 94 DNOQSVIERGAFQDLKQLERLNKLNKQLVPELLFQSTPKLTRLDLSENQIQGPKAF 153
QY 191 KGMNALHVLENSANPLDNG---TEPGAFEG-----VTVF----- 222
DB 154 RGITDVKNLQ-----LDNNHISCIEDGAFRALRDLEILTLNNNITSLIPLSSFNHMPKIR 208
QY 223 -----HIR-----IAEAK----- 230
DB 209 TLRHLSNHLCDCHLAWLSDWLRQRVTGQFTCLCMAPVHLRGFNVDVQKKEYVCAPHS 268
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Itoh A., Miyabayashi T., Ohno M., Sakano S.;  
"Cloning and expressions of three mammalian homologues of Drosophila  
slit suggest possible roles for Slit in the formation and maintenance  
of the nervous system";  
Brain Res. Mol. Brain Res. 62:175-186(1998).

SEQUENCE OF 785-1523 FROM N.A.  
TISSUE=BRAIN;  
MEDLINE=98360089; PubMed=9693030;  
Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;  
"Identification of high-molecular-weight proteins with multiple EGF-  
like motifs by motif-trap screening";  
Genomics 51:27-34(1998).

EMBL; AB0117169; BAA35186.1; -;  
EMBL; AB011538; BAA32466.1; -;  
HSSP; P00740; IEDM.  
InterPro: IPR000152; Asx\_hydroxyl.  
InterPro: IPR000359; Cys\_knot.  
InterPro: IPR000561; EGF-like.  
InterPro: IPR000742; EGF\_2.  
InterPro: IPR001881; EGF\_CA.  
InterPro: IPR003006; Ig\_MHC.  
InterPro: IPR002049; Laminin\_EGF.  
InterPro: IPR001791; Laminin\_G.  
InterPro: IPR001611; LRR.  
InterPro: IPR000483; LRR\_Cterm.  
InterPro: IPR000372; LRR\_Nterm.  
InterPro: IPR003592; LRR\_out.  
InterPro: IPR003591; LRR\_typ.

Pfam: PF00008; EGF; 9.  
Pfam: PF00054; laminin\_G; 1.  
Pfam: PF00560; LRR; 19.  
Pfam: PF01463; LRRCT; 4.  
Pfam: PF01462; LRRNT; 4.  
PRINTS: PR00011; EGF\_LAMININ.  
PRINTS: PR00019; LEURICHRPT.  
SMART: SM00041; CT; 1.  
SMART: SM00179; EGF\_CA; 1.  
SMART: SM00001; EGF\_like; 5.  
SMART: SM00282; LamG; 1.  
SMART: SM00370; LRR; 4.  
SMART: SM00082; LRRCT; 4.  
SMART: SM00013; LRRNT; 4.  
SMART: SM00369; LRR\_TYP; 9.

PROSITE: PS00010; ASX\_HYDROXYL; UNKNOWN\_2.  
PROSITE: PS01185; CTCK\_1; UNKNOWN\_1.  
PROSITE: PS01225; CTCK\_2; 2.  
PROSITE: PS00022; EGF\_1; UNKNOWN\_9.  
PROSITE: PS01186; EGF\_2; 7.  
PROSITE: PS01187; EGF\_CA; 2.  
PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.  
KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.  
SQ SEQUENCE 1523 AA; 167684 MW; 52549D41D1D6DBD1 CRC64;

Db 231 LQNIYLQWNKISVIG-----QTMSWTWSSL-QRLDLSGNEIEAFS-GPSVFCQVPNLQRL 283

QY 371 SV 372

Db 284 NL 285

RESULT 37

Q95K18 PRELIMINARY; PRT; 581 AA.

OS Q95K18:

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Hypothetical 65.9 kDa protein.

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.

OX NCBI\_TaxID=9541;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=TEMPORAL LOBE RIGHT;

RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.

RA Suzuki Y., Sugano S., Hashimoto K.;

RT "Isolation of full-length cDNA clones from macaque brain cDNA libraries."

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AB060846; BAB46868.1; .

DR InterPro: IPR001611; LRR.

DR InterPro: IPR000483; LRR\_Cterm.

DR InterPro: IPR000372; LRR\_Nterm.

DR Pfam: PF00560; LRR; 9.

DR Pfam: PF01463; LRRCT; 1.

DR Pfam: PF01462; LRRNT; 1.

DR SMART: SM00013; LRRNT; 1.

KW Hypothetical protein.

SK SEQUENCE 581 AA; 65880 MW; 8E4F1BBD043669BF CRC64;

Query Match 15.3%; Score 304.5; DB 6; Length 581;

Best Local Similarity 28.8%; Pred. No. 1e-13;

Matches 87; Conservative 57; Mismatches 105; Indels 53; Gaps

QY 74 CPFCQCYSRVYHCDLGLTSVPTNIPDFTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 1332

Db 34 CPKCGRCBGWVYCESQKLOEIPSSISAGCLGLSYRLNSLQKLKYNQFKGLNQLTWLYLD 93

QY 134 NKKLTTHPKAFLTTKKLRILYLSHNLSEIPLNPKSLAEHLIHENKVKKIQKDTFKGM 1933

Db 94 HHNISIDENAFNGIRRLKELLISNSRISYF-LN-----NTFRPV 1732

QY 194 NALHVLMSANPLDNGIEPCAFGVTVFHRTIAEAKLTSVPKGLPTLLEHLHDYNKIS 2533

Db 133 TNLNRLDLSYNQLHSLGE--QFGLR-----KLSLHLWNSLR 1703

QY 254 TVELEDFKRYKELQRLGIGNKNTIDENGSLANIPRVREIHLNKKLKIPSL-PELKY 3123

Db 171 TIPVRFQNCNLELLDGYNRIRSLARNVFNAGMIRKELHLEHNQFSKLNALFPPLVS 2303

QY 313 LQIIFLHNSIARVGVNDPCTVPYKMKKLSYSAISLENNPVKWKEMQPATFRCV--LSRM 3703

Db 231 LQNIYLQWNKISVIG-----QTMSWTWSSL-QRLDLSGNEIEAFS-GPSVFCQVPNLQRL 2833

QY 371 SV 372

Db 284 NL 285

RESULT 38

Q8TF66 PRELIMINARY; PRT; 581 AA.

ID Q8TF66

AC Q8TF66;

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Lib.  
 GN HLIB.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=21645900; PubMed=11785964;  
 RA Satoh K., Hata M., Yokota H.;  
 RT "A Novel Member of the Leucine-Rich Repeat Superfamily Induced in Rat  
 RL Astrocytes by beta-Amyloid."  
 RL Biochem. Biophys. Res. Commun. 290:756-762(2002).  
 DR EMBL: AB071037; BAB84587.1; .  
 SQ SEQUENCE 581 AA; 64396 MW; 1F381485BD2CCB54 CRC64;  
  
 Query Match 14.9%; Score 297.5; DB 4; Length 581;  
 Best Local Similarity 26.4%; Pred. No. 3.2e-13;  
 Matches 100; Conservative 64; Mismatches 134; Indels 81; Gaps 12;  
  
 QY 74 CPFGCQCYSRV--VHCSDLGITSVPTNIPDTRMLDLQNNKIKIKENDPKGLTSLYGLI 131  
 DB 25 CPSECTC-SRASQVECTGARIVATPFPWNAMSLQILNTHITELNESPPLNISALIALR 83  
  
 QY 132 LNNKLTAKIHPKAFLTTKLRLRYLSHNLSEIPLNLPK---SLAELRIHENKVKIKQD 188  
 DB 84 IEKNLSRITPGAPRNLSGLRYLSLANNKQVLPVIGLFOGLDSLESLLSSNQLLOIQA 143  
  
 QY 189 TFGKGNALHYLEMSANPLDNGTEPGAF---GVV-----VFH----- 223  
 DB 144 HFSQCNLKEQLQGNHLEY--IPDGAFLHVLGLTKNLGKSLTHISPRVFOHGLNQV 201  
  
 QY 224 IRIAEAKLTSPKG-----LPP-----TLLEHLVDYKISTVE 256  
 DB 202 LRLYENRLTDPMGTFDGLVNLQELALQOQIGLLSPGLFHHNNHQLRYLSNNHISQLP 261  
  
 QY 257 LEDPKRYELQRLGLGNKTTIDENGSLANIPRVREHLNENKLLKIPGSL-PELKYLQI 315  
 DB 262 PSIFMQLPOLNRLTFLGNSLKLGLSIFGPMNRLRELWLDNHISSLPDVFNLRLQV 321  
  
 QY 316 IFLHSNIAIRGVNDFCTVPKMKKSLYS-----ATSLFNNPVKYWE 357  
 DB 322 LILSRNQLSIFSGAFNGLTELSLHTNALQDLQNGVFRMLANQLNLSQNNRLR--Q 379  
  
 QY 358 MQPATFRVLSRMSVOLGN 376  
 DB 380 LPGNIFANVNGLMALQON 398  
  
 RESULT 39  
 P70193 ID P70193 PRELIMINARY; PRT; 1091 AA.  
 AC P70193;  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Membrane glycoprotein.  
 GN IMG.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96394313; PubMed=8798419;  
 RA Suzuki Y., Sato N., Tohyama M., Wanaka A., Takagi T.;  
 RT "cDNA cloning of a novel membrane glycoprotein that is expressed  
 RT specifically in glial cells in the mouse brain LIG-1: A protein with  
 RT leucine-rich repeats and immunoglobulin-like domains."  
 RL J. Biol. Chem. 271:22522-22527(1996).

DR EMBL: D78572; BAAL1416.1; .  
 DR HSSP; P56276; ITLK.  
 DR MGD; MGI:107935; Img.  
 DR InterPro; IPR003598; Ig\_C2.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR000483; LRR\_Cterm.  
 DR InterPro; IPR000372; LRR\_Nterm.  
 DR InterPro; IPR003592; LRR\_out.  
 DR InterPro; IPR003591; LRR\_type.  
 DR Pfam; PF00047; ig\_3.  
 DR Pfam; PF00560; LRR; 14.  
 DR Pfam; PF01463; LRRCT; 1.  
 DR Pfam; PF01462; LRRNT; 1.  
 DR SMART; SM00408; ICG2; 3.  
 DR SMART; SM00370; LRR; 6.  
 DR SMART; SM00082; LRRCT; 1.  
 DR SMART; SM00013; LRRNT; 1.  
 DR SMART; SM00369; LRR\_Typ; 4.  
 KW Immunoglobulin domain.  
 SQ SEQUENCE 1091 AA; 119283 MW; AL3D0866CE4C203D CRC64;  
  
 Query Match 14.9%; Score 296; DB 11; Length 1091;  
 Best Local Similarity 30.1%; Pred. No. 8.8e-13;  
 Matches 94; Conservative 64; Mismatches 124; Indels 30; Gaps 12;  
  
 QY 74 CPFGCQCYSRVHCSDLGITSVPTNIPDTRMLDLQNNKIKIKENDPKGLTSLYGLIN 133  
 DB 43 CAACTCAGNSLDCSGRLATLPRLPSWTRSLNLSYNRLSEIDSAFEDLTNLQEVYLN 102  
  
 QY 134 NKKLTAKIHPKAFLTTKLRLRYLSHNLSEI---PLNLPKSLAELRIHENKVKIKQD 190  
 DB 103 SNELTAI-PSLTASIGVSVLSFLQHNKILSVDSQSLKSLYLSEVLDLSNNITEIRSCF 161  
  
 QY 191 KGMNALHYLEMSANPLDNGI---EPGAFEGV--TVFHRIAEAKLTSP-KGLP-PTLL 243  
 DB 162 P--NGLRTELN---LASNRISILESGAFDGLSRSLTLRLSKNRITOLPVKAPKLPLT 216  
  
 QY 244 EHLDYNKISTVELEDPKRYELQRLGLGNKTTIDENGSLANIPRVREHLNENKLLK 303  
 DB 217 QLDLNRNRLTLEGITFQGLDSLEVLRLQNNISRLTGDGAFGLSKMHVHLHLEYSLEV 276  
  
 QY 304 PSG-LPELKYLIQILFHSNIAIRGVN--DRCPTVPKMKKSLYSALSLFNNPVKYWE 360  
 DB 277 NGSYGLTALHQLHLSNNSIRIORGWSFC-----QKHELILSFNLTRIDEESL 329  
  
 QY 361 ATRCVLSRMSV 372  
 DB 330 AE---LSLSLI 337  
  
 RESULT 40  
 Q96JAI ID Q96JAI PRELIMINARY; PRT; 1093 AA.  
 AC Q96JAI;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Membrane glycoprotein LIG-1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Nilsson J., Vallbo C., Henriksson R., Hedman H.;  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF381545; AAK62357.1; .  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR000483; LRR\_Cterm.  
 DR InterPro; IPR000372; LRR\_Nterm.

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DR SMART: SM00370; LRR: 5.
DR SMART: SM00082; LRRCT: 1.
DR SMART: SM00013; LRRNT: 1.
DR SMART: SM00369; LRR_TYP: 14.
KW Immunoglobulin domain.
SQ SEQUENCE 1094 AA; 119165 MW; 6B2D0CC3C2783F18 CRC64;

Query Match      14.5%; Score 289; DB 4; Length 1094;
Best Local Similarity 28.5%; Pred. No. 2.8e-12;
Matches 88; Conservative 63; Mismatches 134; Indels 24; Gaps 9;

Qy 74 CPFGCQCYRVVHSCDGLGTSVPINIPDTEMLDQNNKKEIKENDFKGLTSYGLIIN 133
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 41 CAAACTCAGDSLDCGGRGALPGDLPSTRLSNLSYNKLSSEIDPAGFEDLPNQEVYLN 100
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 134 NKKTKIHPKAFLTTKLRRYLYLSHNLSEI--PLNPKSLAEIRIHENKVKKIQKDTF 190
   ||| || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 101 NNELTAV-PSLGAASSHVVSLFLOHKNKTRSEVGSQKAYLSEVLDDLSNNITEVRNCTF 159
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 191 KGMNALHYLEMSANPLDNNGIEPGAFCGV--TVFHIRIAEAKLTSPVKGL--PPTLLEIH 246
   : | : | : | | | | | | | | | | | | | | | | | | | | | | | |
Db 160 PHGPPIKELNLAGNRIGT--LELGAFDGLSRSLTLRLSKNRITQLPVRAFKLPRLTOLD 217
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 247 LDYNKISTVELEDKRYKELQRLGNGNKKITDIENGSLANIPRVREIHLNNKKIIPSG 306
   | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 218 LNRNRIRLIEGTLTFQGLNSLEVLKQLQRNNISKLTGDAFWGLSKMHLVLEYSNVESNG 277
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 307 -LPELKYLIQITFLHSNSIARVGVN--DFCPTVPKMKKSLYSALSIFNPNPVKWEQPATF 363
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 278 SLYGLTALHQLHLSNNSIARHKGWSEF-----QKLHELVLVSFNNLTRLDEESLAE- 329
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 364 RCVLSRMSV 372
   || | | | |
Db 330 ---LSSISV 335

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RESULT 42
Q63156 PRELIMINARY; PRT; 96 AA.
AC O63156;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Decorin (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPAGUE-DAWLEY; TISSUE=LUNG;
RA Moats-Staats B.M., Stiles A.D., Xu L.;
RT "Expression of decorin RNA in rat lung undergoing chronic lung
    injury."
RL Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; L75825; AAA85371.1; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003592; LRR_out.
DR Pfam; PF00560; LRR; 3.
DR SMART; SMO0370; LRR; 2.
FT NON_TER 1
FT TER 1
FT NON_TER 96
FT TER 96
SQ SEQUENCE 96 AA; 10398 MW; C6D19F1750B050D0 CRC64;

Query Match      14.4%; Score 287; DB 11; Length 96;
Best Local Similarity 54.2%; Pred. No. 2.le-13;
Matches 52; Conservative 20; Mismatches 24; Indels 0; Gaps 0;

QY 223 HIRAEAKLTVPKGLPTLEHLHDYNKIISTVELEDPKRYKELORGIGNNKITDIENG 282
| | | | : | : | : | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 YITADTNTISIQGSLPSTELHJDGNKISRVDAAASIKLNNAKLGLSFNSAVDG 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 283 SIANTPIRVRETHLENNKKLKPPSGLPKLYQLIOLIF 318
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Db 144 QFSQSNRLRELQHGNNLESIPAEAFDLVGLTKLNLRNSFTH--LSPRLFQHLGNLQV 201
Q9N4G6
Qy 225 -RIAEAKTSPKPG--LPPTLLLEHLDYNNKISTVELEDFKRYKELQRLGIGNNKITDIE 280
Db 202 LRLHENRUSDIPMGFTFALGNLQALQEOIGTSLPGLFHNNRNQRLYLSNNHISQLP 261
Qy 281 NCSLANIPRVREIHLNNKIKIPSG---LPELKYLIQIIFLHNSNIARVGVNDF 331
Db 262 PGIFMQLPOLNKLTLFGNSLRELSPGVGPMPLNREL--WLYNNHITSLADNTF 313

RESULT 47
Q9N4G6 PRELIMINARY; PRT; 542 AA.
ID Q9N4G6
AC Q9N4G6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Y71F9B.8 protein (ID304).
GN Y71F9B.8 OR ID304.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN None;
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Watson R.;
RT None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RT Science 282:2012-2018(1998).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Watson R.;
RL Submitted (Feb-2000) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Kohara Y., Shin'i T., Suzuki Y., Sugano S., Potdevin M.,
RA Thierry-Mieg Y., Thierry-Mieg D., Thierry-Mieg J.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC024201; AAF36020.1; -.
DR EMBL; AF304125; AAG50238.1; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003592; LRR_Out.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF01463; LRRCT; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00370; LRR; 5.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_TYP; 3.
SQ SEQUENCE 542 AA; 59272 MW; EA5CA06808ADE92E CRC64;

Query Match 14.18; Score 281; DB 5; Length 542;
Best Local Similarity 26.5%; Pred. No. 4.9e-12;
Matches 90; Conservative 61; Mismatches 122; Indels 66; Gaps 10;

Qy 74 CPGCGQYSRVVH-CSDGLGTSVPTNIPFDTRMLDLONNKIKETKENDFKGLTSLYLIL 132
Db 18 COSGCKPCKTAVCKGSSLSRIPILDPRTTVLDLSNNRISRLSADLSLYPNLEQIL 77
Qy 133 NNNKLTIKHPKAFLLTKRLRLYLSHNLSEIP---LNLPSLAELRIHNNKVKIKQDT 189
Db 78 HNSITHTLSADVFSTLPSRLVLDLSSNLSLLPLNEVFSKLNKLTLLTSSNDV-QLGPEC 136
Qy 190 FKGMAHLVLEMSANPLDNNNGIERGAFEGVT-VFHIRTAELKTVSPKGLPPTL--LE-L 245
Db 137 FAGLSQQLTSLADNRL--SFLPPSVLKPGLSLRLNLDLSANKLLSMPASVMNNGLETL 194

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Qy 246 HLDYNNKISTVELEDFKRYKELQRLGIGNNKITDIENGSLANIPRVREIHLNNKIKIP- 304
Db 195 KLQNQLSSLETGMLFSOKELKHLVDSENLIGDIEGALYGLEKLETLNQLNQLVRPG 254
Qy 305 -----SGLPELKYLIQI-----I 316
Db 255 NTWSLPALKTLDLSSNLFVLSLETASFQDGLPALQYLNLSHSNRNKTOMATFVOLSLSHL 314
Qy 317 FLHNSNIARVGVNDFCPTVPKMKKSLYSALSFLNPNVKY 355
Db 315 STSSSALTHIHFSAFNPIPP-----LSHLDSLNNELRY 347

RESULT 48
Q9VFP0 PRELIMINARY; PRT; 1513 AA.
ID Q9VFP0
AC Q9VFP0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CG5195 protein.
GN CG5195
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Randell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazef R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Brill J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA De Carlos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Turner C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AF003591; AAF51605.1; -.
DR FlyBase; FBgn0036995; CG5195.
DR InterPro; IPR002064; DNA_pol_B.

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QY 68 FDLPMCPFG-----CQCYRVVHCSDLGTSVPTNIPEDTRMLDLQNNKIKEIKENDFKG 123
Db 29 FQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPHNLIS-GLLGSLRYNSLSLSELRAGQFTG 87
QY 124 LTSYGLILNKKTKIHPKAFLTTKLRLRLYLSHNOLSEIPLNPKSLAEELRIHENKVK 183
Db 88 LMQLTWLYLDHNHICSVQGDFAFKLRRVKELTSSNQITQLP----- 129
QY 184 KIQKDTFKCMALHVLMSANPLDNNGIEPGAFEGVTVFHIRIAFAKITSVPKGLPTLL 243
Db 130 ---NTFRPMPNLRSDVLSYNKL--QALAPDLFHGL-----RKLT----- 165
QY 244 ELHLDYNNKISTVELEDFKRYKELQRLGLGNKKITDIENGLANIPRVREIHLNKKLKI 303
Db 166 -LHMFRANAIQFVPVRFODCRSLKFLDIGYNQLKSLARNSFAGLFKLTLEHNDLVKV 224
QY 304 P-SGLPELKYLIQIFLHNSIARGVN-DFCPTVPKMKKSLSAISLFNPNVXYWEMOPA 361
Db 225 NFAHFRLLISLHSLCLRRNKVAIVVSSLDWVWNLKEM-----DLSGNEIEY--MEPH 274
QY 362 TPRCVLSRMSVOL 374
Db 275 VEETVPHLQSLQL 287

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